

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 09:00:24 ; Search time 2617 Seconds
(without alignments)
370.311 Million cell updates/sec

Title: US-10-643-801A-35
Perfect score: 20
Sequence: 1 gcatgacacatccatctc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2104966

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Listing first 45 summaries

Database :

GenBdb1:*
1: gb_ba:*
2: gb_hng:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_pl:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	65.0	54	6	AR356488 Sequence
C 2	13	65.0	54	6	AR538044 Sequence
C 3	13	65.0	60	6	COS48380 Sequence
C 4	12	60.0	20	6	AX293633 Sequence
C 5	12	60.0	21	6	AR148756 Sequence
C 6	12	60.0	24	6	AX289000 Sequence
C 7	12	60.0	26	6	AX551638 Sequence
C 8	12	60.0	26	6	AX703273 Sequence
C 9	12	60.0	29	6	AR039144 Sequence
C 10	12	60.0	29	6	AR065274 Sequence
C 11	12	60.0	29	6	BD061658 Sequence
C 12	12	60.0	39	6	AR128133 Sequence
C 13	12	60.0	51	6	AX116213 Sequence
C 14	12	60.0	51	6	AX159371 Sequence
C 15	12	60.0	51	6	AX159372 Sequence
C 16	12	60.0	51	6	AX159373 Sequence
C 17	12	60.0	51	6	AX165283 Sequence
C 18	12	60.0	55	11	HOMUT5280A
C 19	12	60.0	60	6	COS45434 Sequence

20	12	60.0	60	6	COS47633 Sequence
21	12	60.0	66	9	AY139609 Homo sapi
22	11	55.0	17	6	AR040149 Sequence
C 23	11	55.0	18	6	AR241626 Sequence
C 24	11	55.0	18	6	AR258715 Sequence
C 25	11	55.0	18	6	AX137953 Sequence
C 26	11	55.0	18	6	BD015843 DNA encod
C 27	11	55.0	19	6	AR174747 Sequence
C 28	11	55.0	20	6	A82791 Sequence 4
C 29	11	55.0	20	6	A83708 Sequence 4
C 30	11	55.0	20	6	BD274392 Human van
C 31	11	55.0	20	6	C0757498 Sequence
C 32	11	55.0	20	6	AX026882 Sequence
C 33	11	55.0	20	6	BD082732 Intracell
C 34	11	55.0	21	6	CQ831007 Sequence
C 35	11	55.0	21	6	AX077873 Sequence
C 36	11	55.0	22	6	BD102253 Method of
C 37	11	55.0	22	6	AX166683 Sequence
C 38	11	55.0	25	6	AX196821 Sequence
C 39	11	55.0	25	6	BD140471 Secreted
C 40	11	55.0	29	6	BD191485 Secreted
C 41	11	55.0	30	6	AX537725 Sequence
C 42	11	55.0	31	6	CQ868121 Sequence
C 43	11	55.0	36	6	AX512846 Sequence
C 44	11	55.0	42	6	AR021384 Sequence
C 45	11	55.0	42	6	AR042946 Sequence

ALIGNMENTS

RESULT 1
AR356488/c
LOCUS AR356488 54 bp DNA
DEFINITION Sequence 2606 from patent US 6593114.
ACCESSION AR356488
VERSION AR356488.1 GI:33762572
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and Rosen,C.A.
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 2606 15-JUN-2003;
FEATURES
source
1..54
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 55.0%; Score 13; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 3,4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCCAT 16
Db 47 TTGGCACTCCCAT 35

RESULT 2
AR538044/c
LOCUS AR538044 54 bp DNA
DEFINITION Sequence 2606 from patent US 6737248.
ACCESSION AR538044
VERSION AR538044.1 GI:53929261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and

TITLE Rosen, C.A.
JOURNAL Staphylococcus aureus polynucleotides and sequences
FEATURES Patent: US 6737248-A 2606 18-MAY-2004;
SOURCE Location/Qualifiers
1..54
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGCCACTCCCAT 16
Db 47 TTGCCACTCCCAT 35

RESULT 3
COS48380
LOCUS Sequence 18015 from Patent WO0210449.
DEFINITION COS48380
ACCESSION CQ548380.1 GI:41514807
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
FEATURES Patent: WO 0210449-A 18015 07-FEB-2002;
SOURCE Inc. (US)
Location/Qualifiers
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGCCACTCCCAT 16
Db 4 TTGCCACTCCCAT 16

RESULT 4
AX293633/c
LOCUS AX293633 20 bp DNA
DEFINITION Sequence 5395 from Patent WO0179548.
ACCESSION AX293633
VERSION AX293633.1 GI:17055316
KEYWORDS
SOURCE
ORGANISM
FEATURES
1 synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Barany, F., Zivyl, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
FEATURES Patent: WO 0179548-A 5395 25-OCT-2001;
SOURCE CORNELL RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTC 12
Db 15 GCATTGCCACTC 4

RESULT 5
ARI48756
LOCUS ARI48756 21 bp DNA
DEFINITION Sequence 113 from patent US 6225451.
ACCESSION ARI48756
VERSION ARI48756.1 GI:15112846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 21)
Baillinger, D.G., Ding, W., Wagner, S. and Hess, M.A.
TITLE Chromosome 11-linked coronary heart disease susceptibility gene
JOURNAL CHD1
FEATURES Patent: US 6225451-A 113 01-MAY-2001;
SOURCE Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGCCACTCCCA 15
Db 2 TTGCCACTCCCA 13

RESULT 6
AX289000/c
LOCUS AX289000 24 bp DNA
DEFINITION Sequence 762 from Patent WO0179548.
ACCESSION AX289000
VERSION AX289000.1 GI:17050683
KEYWORDS
SOURCE
ORGANISM
FEATURES
1 synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Barany, F., Zivyl, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
FEATURES Patent: WO 0179548-A 762 25-OCT-2001;
SOURCE CORNELL RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTC 12
Db 19 GCATTGCCACTC 8

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RESULT 7
AX551638          26 bp  DNA          linear  PAT 26-NOV-2002
LOCUS
DEFINITION      Sequence 257 from Patent WO0250276.
ACCESSION      AX551638
VERSION        AX551638.1  GI:25814437
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1. Li, L., Padigaru, M., Ballinger, R.A., Kekuda, R., Colman, S.D.,
  Sciore, P., Smithson, G., Peyman, J.A., Macdougall, J.R., Stone, D.,
  Vernet, C.A., Shenoy, S., Gunther, E., Millet, I., Tchernev, V.T.,
  Anderson, D., Gusev, V., Malyanekar, U.M., Zhong, H., Ellerman, K.E. and
  Wolanc, A.
  Novel proteins and nucleic acids encoding same
  Patent: WO 0250276-A 257 27-JUN-2002;
  Curagen Corporation (US)
FEATURES
source
1..26
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/notes="Taqman PCR primer"

ORIGIN
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
4 TTGGCACTCCCA 15
|||||
5 TTGGCACTCCCA 16

Db

RESULT 8
AX703273          26 bp  DNA          linear  PAT 03-APR-2003
LOCUS
DEFINITION      Sequence 502 from Patent WO02055313.
ACCESSION      AX703273
VERSION        AX703273.1  GI:29538319
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1. Li, L., Ballinger, R.A., Padigaru, M., Kekuda, R., Colman, S.D.,
  Spytek, R.A., Casman, S.J., Vernet, C.A., Shenoy, S.G., Gusev, V.,
  Malyanekar, U.M., Edinger, S., Gerlach, V., Smithson, G., Stone, D.J.,
  Sciore, P., Macdougall, J.R., Gunther, E., Peyman, J.A., Ellerman, K.,
  Gangoli, E.A. and Millet, I.
  G-protein coupled receptors and nucleic acids encoding same
  Patent: WO 02059313-A 502 01-AUG-2002;
  Curagen Corporation (US)
FEATURES
source
1..26
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/notes="PCR Primer Sequence"

ORIGIN
Query Match      60.0%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
4 TTGGCACTCCCA 15
|||||
5 TTGGCACTCCCA 16

Db

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RESULT 9
AR039144/c        29 bp  DNA          linear  PAT 29-SEP-1999
LOCUS
DEFINITION      Sequence 8 from patent US 5807740.
ACCESSION      AR039144
VERSION        AR039144.1  GI:5958507
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1. Amaral, M. Catherine, and Chen, J.-L.
  Regulators of UCP2 gene expression
  Patent: US 5807740-A 8 15-SEP-1999;
  Location/Qualifiers
  1..29
/mol_type="unknown"

ORIGIN
Query Match      60.0%; Score 12; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
4 TTGGCACTCCCA 15
|||||
20 TTGGCACTCCCA 9

Db

RESULT 10
AR065274/c        29 bp  DNA          linear  PAT 29-SEP-1999
LOCUS
DEFINITION      Sequence 8 from patent US 5849514.
ACCESSION      AR065274
VERSION        AR065274.1  GI:5995490
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1. Amaral, M. Catherine, and Chen, J.-L.
  Method of identifying agents that modulate UCP2 promoter activity
  Patent: US 5849514-A 8 15-DEC-1998;
  Location/Qualifiers
  1..29
/mol_type="unknown"

ORIGIN
Query Match      60.0%; Score 12; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
4 TTGGCACTCCCA 15
|||||
20 TTGGCACTCCCA 9

Db

RESULT 11
BD061658/c        29 bp  DNA          linear  PAT 27-AUG-2002
LOCUS
DEFINITION      Regulators of UCP2 gene expression.
ACCESSION      BD061658
VERSION        BD061658.1  GI:22607263
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1. Amaral, C.M. and Chen, J.L.
  Regulators of UCP2 gene expression
  Patent: JP 2001507943-A 8 19-JUN-2001;
  TULARIK INC

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COMMENT      PN      JP 2001507943-A/8
              PD      19-JUN-2001
              PF      22-APR-1998 JP 1998547120
              PR      25-APR-1997 US 08/846012
              PI      CATHERINE M AMARAL, JIN LONG CHEN
              PC      C12N1/00, C12N5/10, C12N15/11, C12N15/63, C12Q1/02, C12Q1/68 CC
              Strandedness: Double;
              CC      Topology: Linear;
              PH      Key      Location/Qualifiers.
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              /db_xref="taxon:32630"
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Query Match      60.0%; Score 12; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 TTGCCACTCCCA 15
              |||||
              20 TTGCCACTCCCA 9
Db
RESULT 12
ARI28133/c      ARI28133      39 bp      DNA      linear      PAT 16-MAY-2001
LOCUS      DEFINITION      Sequence 8 from patent US 6183956.
ACCESSION      ARI28133
VERSION      ARI28133.1 GI:14115795
KEYWORDS
SOURCE      unknown.
ORGANISM      unknown.
REFERENCE
  AUTHORS      1 (bases 1 to 39)
  TITLE      Sivaraja.M., Strulovici.B. and Flores.O.A.
  JOURNAL      High throughput in vitro screening assays for transcription
  FEATURES
    source      Location/Qualifiers
                1..39
                /organism="unknown"
                /mol_type="unassigned DNA"
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Query Match      60.0%; Score 12; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      8 CACTCCCATCTCT 19
              |||||
              27 CACTCCCATCTCT 16
Db
RESULT 13
AX116213
LOCUS      AX116213      51 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION      Sequence 1336 from Patent WO0129262.
ACCESSION      AX116213
VERSION      AX116213.1 GI:14033155
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  AUTHORS      1
  TITLE      Picoult-Newburg, L. and Pohl, M.
  JOURNAL      Genotyping reagents, kits and methods of use thereof
  FEATURES
    source      Location/Qualifiers
                1..51
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
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                /note="1 of 2 allelic variants (2700 is other entry)"
ORIGIN
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 TGCCACTCCCAT 16
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              45 TGCCACTCCCAT 34
Db
RESULT 14
AX159371/c      AX159371      51 bp      DNA      linear      PAT 22-JUN-2001
LOCUS      DEFINITION      Sequence 2699 from Patent WO0140521.
ACCESSION      AX159371
VERSION      AX159371.1 GI:14540702
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  AUTHORS      1
  TITLE      Shinketsu, R.A. and Leach, M.
  JOURNAL      Nucleic acids containing single nucleotide polymorphisms and
  FEATURES
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                /note="1 of 2 allelic variants (2700 is other entry)"
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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 TGCCACTCCCAT 16
              |||||
              45 TGCCACTCCCAT 34
Db
RESULT 15
AX159372/c      AX159372      51 bp      DNA      linear      PAT 22-JUN-2001
LOCUS      DEFINITION      Sequence 2700 from Patent WO0140521.
ACCESSION      AX159372
VERSION      AX159372.1 GI:14540703
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  AUTHORS      1
  TITLE      Shinketsu, R.A. and Leach, M.
  JOURNAL      Nucleic acids containing single nucleotide polymorphisms and
  FEATURES
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ORIGIN

/note="2 of 2 allelic variants (2699 is other entry)
Accession number CG42330545"

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCAT 16
|||||
Db 45 TGGCACTCCCAT 34

RESULT 16

AX159373/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX159373
DEFINITION Sequence 2701 from Patent WO0140521.
ACCESSION AX159373
VERSION AX159373.1 GI:14540704
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2701 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/note="1 of 2 allelic variants (2702 is other entry)
Accession number CG42330545"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCAT 16
|||||
Db 35 TGGCACTCCCAT 24

RESULT 17
AX165283/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX165283
DEFINITION Sequence 478 from Patent WO0138586.
ACCESSION AX165283
VERSION AX165283.1 GI:14546112
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 478 31-MAY-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
26
/note="single nucleotide polymorphism

ORIGIN

Accession number CG44005525"

Query Match 60.0%; Score 12; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGCCACTC 12
|||||
Db 27 GCATTGCCACTC 16

RESULT 18

HUMUT5280A 55 bp DNA linear STS 28-DEC-1994
LOCUS HUMUT5280A
DEFINITION Human STS UT5280, 5' primer bind, sequence tagged site.
ACCESSION L30822
VERSION L30822.1 GI:604659
KEYWORDS STS; PCR primer; STS sequence; microsatellite DNA; microsatellite
marker; mononucleotide repeat; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Gerken, S.C., Matsunami, N., Plautke, R., Albertsen, H., Ballard, L.,
Wells, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X.,
Robertson, M., Bradley, P., Elner, T., Tingey, A., Lalouel, J.-M. and
White, R.
TITLE Genetic and physical mapping of simple sequence repeat containing
sequence tagged sites from the human genome
JOURNAL Unpublished (1994)
COMMENT Original source text: Homo sapiens DNA.
Submitted by: Utah Center for Human Genome Research University of
Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: stecorona.med.utah.edu
Primer A: CACTCAGCCTGGGCAATTAAG
Primer B: GTAGCTCTGTTGCACATGACACT
PCR Profile:
Initial Denaturation: 94C 300sec
Cycles Denaturation Annealing Extension 94 94
C 10 sec. 60 C 10 sec. 72 C 20 sec. 30
70 C 10 sec. 72 C 20 sec. Mg++: 1.50 mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 3.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ORIGIN

Query Match 60.0%; Score 12; DB 11; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CATTGCCACTCC 13
|||||
Db 5 CATTGCCACTCC 16

RESULT 19

CQ545434/c 60 bp DNA linear PAT 30-JAN-2004
LOCUS CQ545434
DEFINITION Sequence 15069 from Patent WO0210449.
ACCESSION CQ545434
VERSION CQ545434.1 GI:41511698
KEYWORDS

Source	Homo sapiens (human)
Organism	Homo sapiens
Reference	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Authors	Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
Title	Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcripome
Journal	Patent: WO 0210449-A 15069 07-FEB-2002;
Features	CompuGen Inc. (US)
Source	Location/Qualifiers
Origin	1. 60 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	60.0%; Score 12; DB 6; Length 60;
Best Local Similarity	100.0%; Pred. No. 1.4e+04;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	9 ACTCCCATCTT 20
Db	17 ACTCCCATCTT 6
Result 20	CQ547633 60 bp DNA PAT 30-JAN-2004
LOCUS	CQ547633
DEFINITION	Sequence 17268 from Patent WO0210449.
ACCESSION	CQ547633
VERSION	CQ547633.1 GI:41513897
KEYWORDS	
Source	Homo sapiens (human)
Organism	Homo sapiens
Reference	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Authors	Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
Title	Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcripome
Journal	Patent: WO 0210449-A 17268 07-FEB-2002;
Features	CompuGen Inc. (US)
Source	Location/Qualifiers
Origin	1. 60 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	60.0%; Score 12; DB 6; Length 60;
Best Local Similarity	100.0%; Pred. No. 1.4e+04;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GCATTGCCACTC 12
Db	44 GCATTGCCACTC 55
Result 21	AY139609 66 bp DNA PRI 21-OCT-2002
LOCUS	AY139609
DEFINITION	Homo sapiens dytstrophin (DMD) gene deletion breakpoint junction 04.
ACCESSION	AY139609
VERSION	AY139609.1 GI:24209751
KEYWORDS	
Source	Homo sapiens (human)
Organism	Homo sapiens
Reference	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Authors	Shihori,M., Pozzoli,U., Cagliani,R., Giorda,R., Comi,G.P., Bardon,A., Menozzi,G. and Bresolin,N.
Title	Relevance of sequence and structure elements for deletion events in the dystrophin gene major hot-spot
Journal	Unpublished
Authors	2 (bases 1 to 66)
Source	Submitted (06-AUG-2002) I.R.C.C.S. E.Medea, Ass. La Nostra Famiglia, Via Don L. Monza, 20, Bobbio Parini, LC 23842, Italy
Features	Location/Qualifiers
Source	1. 66 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
Gene	<1. .>66 /gene="DMD" /note="dystrophin"
Intron	<1. .30 /gene="DMD" /number=44
Misc_recomb	31. .35 /gene="DMD" /note="deletion breakpointjunction 04"
Intron	36. .>66 /gene="DMD" /number=48
Origin	
Query Match	60.0%; Score 12; DB 9; Length 66;
Best Local Similarity	100.0%; Pred. No. 1.3e+04;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	9 ACTCCCATCTT 20
Db	48 ACTCCCATCTT 59
Result 22	AR040149 17 bp DNA PAT 29-SEP-1999
LOCUS	AR040149
DEFINITION	Sequence 997 from patent US 5807743.
ACCESSION	AR040149
VERSION	AR040149.1 GI:5959512
KEYWORDS	
Source	Unknown.
Organism	Unknown.
Reference	Unclassified.
Authors	1 (bases 1 to 17)
Title	Stinchcomb,D.T. and McSwigen,J.A.
Journal	Interleukin-2 receptor gamma-chain ribozymes
Features	Patent: US 5807743-A 997 15-SEP-1998;
Source	Location/Qualifiers
Origin	1. 17 /organism="unknown" /mol_type="unassigned DNA"
Query Match	55.0%; Score 11; DB 6; Length 17;
Best Local Similarity	100.0%; Pred. No. 6e+04;
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2 CATTGCCACTC 12
Db	6 CATTGCCACTC 16
Result 23	AR241626 18 bp DNA PAT 20-DEC-2002
LOCUS	AR241626
DEFINITION	Sequence 5 from patent US 6471964.
ACCESSION	AR241626
VERSION	AR241626.1 GI:27287383
KEYWORDS	

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Biering, E. and Krososoy, B.
TITLE DNA encoding structural protein-1 of infectious Salmon Anaemia virus and uses thereof
JOURNAL Patent: US 6471964-A 5 29-OCT-2002;
FEATURES
source
1. 18
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCA 15
Db 15 TGGCACTCCCA 5

RESULT 24
AR258715/c 18 bp DNA linear PAT 20-DEC-2002
LOCUS AR258715
DEFINITION Sequence 5 from patent US 6489163.
ACCESSION AR258715
VERSION AR258715.1 GI:27309121
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Roy, A.K. and Chen, S.
TITLE Ribozyme mediated inactivation of the androgen receptor
JOURNAL Patent: US 6489163-A 5 03-DEC-2002;
FEATURES
source
1. 18
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCA 15
Db 13 TGGCACTCCCA 3

RESULT 25
AX137953/c 18 bp DNA linear PAT 30-MAY-2001
LOCUS AX137953
DEFINITION Sequence 5 from Patent EPI094069.
ACCESSION AX137953
VERSION AX137953.1 GI:14274051
KEYWORDS Infectious salmon anemia virus
SOURCE Infectious salmon anemia virus
ORGANISM Infectious salmon anemia virus
REFERENCE 1
AUTHORS Biering, E. and Krososoy, B.
TITLE Dna encoding structural protein-1 of infectious salmon anaemia virus and uses thereof
JOURNAL Patent: EP 1094069-A 5 25-APR-2001;
FEATURES
source
1. 18
/organism="Infectious salmon anemia virus"
/mol_type="unassigned DNA"

ORIGIN primer_bind /db_xref="taxon:55987"
1. 18
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCA 15
Db 15 TGGCACTCCCA 5

RESULT 26
BD015843/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS BD015843
DEFINITION DNA encoding structure protein-1 of infectious salmon anaemia virus and utilization thereof.
ACCESSION BD015843
VERSION BD015843.1 GI:22556980
KEYWORDS JP 2001211888-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Eric, B.A. and Beyorn, K.B.
TITLE DNA encoding structure protein-1 of infectious salmon anemia virus and utilization thereof
JOURNAL Patent: JP 2001211888-A 2 07-AUG-2001;
COMMENT AKZO NOBEL NV
OS Infectious salmon anaemia virus
PN JP 2001211888-A/2
PD 07-AUG-2001
PF 17-OCT-2000 JP 2000316583
PR 18-OCT-1999 EP 99203401.7
PI BILLING A ERIC KLOSSEI B BEYORN
PC C12N15/09, A61K38/00, A61K39/145, A61P31/12, C07K14/11, C07K16/10,
PC C12Q1/68,
PC G01N33/569//C12P21/08, C12N15/00, A61K37/02
CC DNA encoding structure protein-1 of infectious salmon anemia virus and
CC utilization thereof
CC FH Key Location/Qualifiers
FT primer_bind (1)..(18).
FEATURES
source
1. 18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 55.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCA 15
Db 15 TGGCACTCCCA 5

RESULT 27
AR174747 19 bp DNA linear PAT 17-DEC-2001
LOCUS AR174747
DEFINITION Sequence 46 from patent US 6307035.
ACCESSION AR174747
VERSION AR174747.1 GI:17915067
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Rauscher, F.J. III and Jensen, D.E.
TITLE BRCA1 associated polynucleotide (BAP-1) and uses therefor

JOURNAL Patent: US 6307035-A 46 23-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 ORIGIN /mol_type="unassigned DNA"

Query Match 55.0%; Score 11; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACCTCCCAT 17
 |||||
 Db 6 CCACCTCCCAT 16

RESULT 28
 A82791/c 20 bp DNA linear PAT 21-JAN-2000

LOCUS A82791 Sequence 4 from Patent EP0884385.
 DEFINITION A82791
 ACCESSION A82791
 VERSION A82791.1 GI:6732470

KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Riccardi, C.

TITLE Intracellular modulators of apoptotic cell death pathways
 JOURNAL Patent: EP 0884385-A 4 16-DEC-1998;
 APPLIED RESEARCH SYSTEMS (AN)

FEATURES Location/Qualifiers
 source 1..20
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGCCACTCCCA 15
 |||||
 Db 18 TGCCACTCCCA 8

RESULT 29
 A83708/c 20 bp DNA linear PAT 21-JAN-2000

LOCUS A83708 Sequence 4 from Patent WO9849291.
 DEFINITION A83708
 ACCESSION A83708
 VERSION A83708.1 GI:6732944

KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Riccardi, C.

TITLE INTRACELLULAR GLUCOCORTICOID-INDUCED LEUCINE ZIPPER MODULATORS OF
 JOURNAL APOPTIC CELL DEATH PATHWAYS
 Patent: WO 9849291-A 4 05-NOV-1998;
 RICCARDI CARLO (IT); APPLIED RESEARCH SYSTEMS (NL)

FEATURES Location/Qualifiers
 source 1..20
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGCCACTCCCA 15
 |||||
 Db 18 TGCCACTCCCA 8

RESULT 30
 BD274392 20 bp DNA linear PAT 17-JUL-2003

LOCUS BD274392 Human vanilloid receptor and use thereof.
 DEFINITION BD274392
 ACCESSION BD274392.1 GI:33084160
 VERSION BD274392.1 GI:33084160

KEYWORDS JP 2002531085-A/29.
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 20)
 AUTHORS Delany, N.S., Sansau, P. and Tate, S.N.
 TITLE Human vanilloid receptor and use thereof
 JOURNAL Patent: JP 2002531085-A 29 24-SEP-2002;
 GLAXO GROUP LTD

COMMENT OS Artificial Sequence
 PN JP 2002531085-A/29
 PD 24-SEP-2002
 PF 30-NOV-1999 JP 2000585397
 PR 01-DEC-1998 GB 9826359.3
 PI NATALIE SAMANTHA DELANY, PHILIPPE SANSEAU, SIMON NICHOLAS TATE

PC C12N15/09,A61K45/00,A61P1/00,A61P11/06,A61P13/00, PC
 A61P19/00,
 PC A61P25/04,A61P25/06,A61P25/28,A61P29/00,A61P29/00,C07K14/705,
 PC C07K16/28,
 PC C12N5/10,C12P21/02,C12Q1/02/(C12P21/02,C12R1:91),C12N15/00,
 PC C12N5/00
 CC Description of Artificial Sequence: Primer
 FH Key
 FT source 1..20
 Location/Qualifiers

FEATURES Location/Qualifiers
 source 1..20
 /organism="Artificial Sequence".
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCCTCTCTT 20
 |||||
 Db 5 CTCCTCTCTT 15

RESULT 31
 CQ757498/c 20 bp DNA linear PAT 01-MAR-2004

LOCUS CQ757498 Sequence 9 from Patent WO2003107249.
 DEFINITION CQ757498
 ACCESSION CQ757498
 VERSION CQ757498.1 GI:44847536

KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE 1
 AUTHORS Kotani, H. and Mizunari, S.
 TITLE Method for predicting a drug transport capability by abcg2
 JOURNAL polymorphisms
 Patent: WO 2003107249-A 9 24-DEC-2003;
 BANYU PHARMACEUTICAL CO., LTD. (JP)

FEATURES Location/Qualifiers
 source 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 55.0%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN /db_xref="taxon:32630"
/note="Exon 4 forward primer"

Query Match 55.0%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CTCGCATTCTT 20
18 CTCGCATTCTT 8
Db 18 CTCGCATTCTT 8

RESULT 32
AX026882 20 bp DNA linear PAT 16-SEP-2000
LOCUS Sequence 35 from Patent WO0032766.
DEFINITION AX026882
ACCESSION AX026882 GI:10187981
VERSION
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Delany,N.S., Tate,S.N. and Sasseau,P.
TITLE Human vanilloid receptors and their uses
JOURNAL Patent: WO 0032766-A 35 08-JUN-2000;
DELANY NATALIE SAMANTHA (GB) ; TATE SIMON NICHOLAS (GB) ; GLAXO
GROUP LTD (GB) ; SANSEAU PHILIPPE (GB)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTCGCATTCTT 20
5 CTCGCATTCTT 15
Db 5 CTCGCATTCTT 15

RESULT 33
BD082732/c 20 bp DNA linear PAT 27-AUG-2002
LOCUS BD082732
DEFINITION Intracellular modulator in apoptosis cell death pathway.
ACCESSION BD082732
VERSION BD082732.1 GI:22628342
KEYWORDS JP 2001523102-A/3.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Riccardi,C.
TITLE Intracellular modulator in apoptosis cell death pathway
JOURNAL Patent: JP 2001523102-A 3 20-NOV-2001;
APPLIED RESEARCH SYSTEMS ARS HOLDING NV
COMMENT OS Mus sp. (mouse)
PN JP 2001523102-A/3
PD 20-NOV-2001
PF 27-APR-1998 JP 1998546599
PR 28-APR-1997 EP 97107033.9
PI CARLO RICCARDI
PC C12N15/12,C07K14/47,G01N33/50,A61K38/17,A61K48/00,C12N5/10 CC
PER reverse primer Location/Qualifiers
FH Key Location/Qualifiers
1..20

FEATURES
source 1..20

ORIGIN /organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"

Query Match 55.0%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGGCACTCCCA 15
18 TGGCACTCCCA 8
Db 18 TGGCACTCCCA 8

RESULT 34
CO831007 21 bp DNA linear PAT 29-JUL-2004
LOCUS CO831007
DEFINITION Sequence 92 from Patent EP1437417.
ACCESSION CO831007
VERSION CO831007.1 GI:50831142
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Park,J.G., Kim,I.J., Kang,H.C. and Park,J.H.
TITLE Beta-catenin oligonucleotide microchip and method for detecting
JOURNAL beta-catenin mutations employing same
National Cancer Center (KR)
Patent: EP 1437417-A 92 14-JUL-2004;
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
4 TGGCACTCCCA 14
Db 4 TGGCACTCCCA 14

RESULT 35
AX077873/c 21 bp DNA linear PAT 22-FEB-2001
LOCUS AX077873
DEFINITION Sequence 29 from Patent WO0105957.
ACCESSION AX077873
VERSION AX077873.1 GI:13157720
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Good,X.C. and Monte,J.
TITLE Grapevine leafroll-associated virus proteins
JOURNAL Patent: WO 0105957-A 29 25-JAN-2001;
AGRIOTPE, INC. (US)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      9 ACTCCATCTT 19
Db      18 ACTCCATCTT 8

RESULT 36
LOCUS   BD102253
DEFINITION
ACCESSION BD102253
VERSION   BD102253.1
KEYWORDS  WO 0171032-A/16.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
           1 (bases 1 to 22)
           Nagano,M., Ito,M., Sagenashi,Y., Hattori,H., Egashira,T.,
           Yamashita,S. and Matsuzawa,Y.
           Method of detecting risk factor for onset of arteriosclerosis
           Patent: WO 0171032-A 16 27-SEP-2001;
           BML INC, MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGEHASHI, HIROAKI HATTORI,
           TORU EGASHIRA, SHIZUYA YAMASHITA, YUJI MATSUZAWA
COMMENT   OS Homo sapiens (human)
           PN WO 0171032-A/16
           PD 27-SEP-2001
           PF 23-MAR-2001
           PI 24-MAR-2000 JP 00P 084264
           PI MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGEHASHI, HIROAKI HATTORI, TORU

FEATURES
SOURCE    1..22
           /organism="Homo sapiens (human)"
           /mol_type="genomic DNA"
           /db_xref="taxon:9606"

ORIGIN
Query Match      55.0%; Score 11; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      5 TGCCACTCCCA 15
Db      1 TGCCACTCCCA 11

RESULT 37
LOCUS   AX166683/c
DEFINITION
ACCESSION AX166683
VERSION   AX166683.1
KEYWORDS  GI:14546958
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE
AUTHORS   1
           Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
           Flanagan,P. and Clary,D.S.
           Novel human protein kinases and protein kinase-like enzymes
           Patent: WO 0138503-A 174 31-MAY-2001;
           Sugen, Inc. (US)
COMMENT   Location/Qualifiers
           1..25
           /organism="synthetic construct"
           /mol_type="unassigned DNA"

OY      9 ACTCCATCTT 19
Db      18 ACTCCATCTT 8

RESULT 38
LOCUS   AX196821
DEFINITION
ACCESSION AX196821
VERSION   AX196821.1
KEYWORDS  GI:15387027
SOURCE    Glycine max (soybean)
ORGANISM  Glycine max
REFERENCE
AUTHORS   Hauge,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.
           Cysteine acid molecules and other molecules associated with soybean
           Patent: WO 0151627-A 528 19-JUL-2001;
           MONSANTO COMPANY (US)
COMMENT   Location/Qualifiers
           1..25
           /organism="Glycine max"
           /mol_type="unassigned DNA"
           /db_xref="taxon:3847"
           /note="Seq ID: 240017_region_G3_35078_13_Reverse_Primer"

ORIGIN
Query Match      55.0%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      10 CTCCCATCTT 20
Db      1 CTCCCATCTT 11

RESULT 39
LOCUS   BD140471
DEFINITION
ACCESSION BD140471
VERSION   BD140471.1
KEYWORDS  GI:23235416
SOURCE    JP 2002506611-A/21.
ORGANISM  synthetic construct
REFERENCE
AUTHORS   1 (bases 1 to 29)
           Jacobs,K., McCoy,J.M., Lavalite,E.R., Racie,L.A.C., Evans,C.,
           Werberg,D., Treacy,M., Agostino,M.J., Il,R.J.S., Wong,G.G.,
           Clark,H.F. and Pechel,K.
           Secreted proteins and polynucleotides encoding them
           Patent: JP 2002506611-A 21 05-MAR-2002;
           GENETICS INSTITUTE INC
COMMENT   OS Artificial Sequence
           PN JP 2002506611-A/21
           PD 05-MAR-2002
           PF 24-NOV-1998 JP 2000522118
           PR 26-NOV-1997 US 60/066804 23-NOV-1998 US 09/197886 PI
           KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALITE, LISA A COLLINS PI
           RACIE,

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PI CHERYL EVANS, DAVID MERBERG, MAURICE TREACY, MICHAEL J AGOSTINO,
PI ROBERT J STEININGER II, GORDON G WONG, HILARY F CLARK, KIM PI
FECHTEL
PC C12N15/09, C07K14/00, C12N1/21, C12N5/10, C12P19/34, C12P21/02, PC
C12Q1/68//
PC A61P29/00, A61P35/00, A61P37/04, A61P37/06, C12N15/00, C12N5/00 CC
oligonucleotide
CC biotinylated phosphoramidite residue
FH Key Location/Qualifiers
FT misc feature (2).
Location/Qualifiers
1..29
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES

source

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGCACTCCCA 15
|||||
DB 8 TGGCACTCCCA 18

RESULT 40
BD191485 29 bp DNA linear PAT 17-JUL-2003

LOCUS BD191485
DEFINITION Secreted proteins and polynucleotides encoding them.
ACCESSION BD191485
VERSION BD191485.1 GI:33001224
KEYWORDS JP 2002510196-A/12.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 29)
AUTHORS Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
Treacy, M., Spaulding, V. and Agostino, M.J.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: JP 2002510196-A 12 02-APR-2002;
COMMENT GENETICS INSTITUTE INC
PN JP 2002510196-A/12
PD 02-APR-2002
PF 14-APR-1998 JP 1998544380
PR 15-APR-1997 US 08/843374.13-APR-1998 US 09/059487 PI
KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
DAVID MERBERG,

PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C07K14/47, A61K38/17

CC Strandedness: Single;
CC Topology: linear;
CC /desc=Oligonucleotide;
FH Key Location/Qualifiers

FEATURES

source

1..29
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACT 11
|||||
DB 14 GCATTGCCACT 24

RESULT 41
AX537725/c
LOCUS AX537725

30 bp DNA linear PAT 23-NOV-2002

DEFINITION Sequence 4 from Patent WO02072845.

ACCESSION AX537725
AX537725.1 GI:25269719

KEYWORDS

SOURCE

synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Chatfield, S.N.

AUTHORS Salmonella promoter for heterologous gene expression
TITLE Patent: WO 02072845-A 4 19-SEP-2002;
JOURNAL Microscience Limited (GB)

FEATURES

Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCACTC 12
|||||
DB 23 CATTGCCACTC 13

RESULT 42

LOCUS CQ868121

31 bp DNA linear PAT 13-SEP-2004

DEFINITION Sequence 338 from Patent WO2004074318.
ACCESSION CQ868121
VERSION CQ868121.1 GI:51998173
KEYWORDS

SOURCE

ORGANISM synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Dautry-Varstat, A. and Subtil-Sands, A.

AUTHORS Secreted chlamydia polypeptides, polynucleotides coding
TITLE therefor, therapeutic and diagnostic uses thereof
JOURNAL Patent: WO 2004074318-A 338 02-SEP-2004;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
(CNRS) (FR)

COMMENT

FEATURES

Location/Qualifiers
1..31
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTCGCATTCTT 20
|||||
DB 18 CTCGCATTCTT 28

RESULT 43
AX512846

36 bp DNA linear PAT 03-OCT-2002

LOCUS AX512846

Sequence 1 from Patent WO02062943.

ACCESSION AX512846

VERSION AX512846.1 GI:23504029

KEYWORDS

SOURCE

ORGANISM

synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Malvy, C., Maksimenko, A.C. and Gottikh, M.
 TITLE Use of oligonucleotides for improving plasmid transfection in
 cells, transfection method and kit
 JOURNAL Patent: WO 02062943-A 1 15-AUG-2002;
 CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR); INSTITUT
 GUSTAVE ROUSSY (FR)

FEATURES
 source Location/Qualifiers
 1..36
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 5.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATTGCCACTCC 13
 |||||
 Db 24 ATTGCCACTCC 34

RESULT 44
 LOCUS AR021384 42 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 32 from patent US 5789650.
 ACCESSION AR021384
 VERSION AR021384.1 GI:3975999

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 42)
 AUTHORS Lonberg, N. and Kay, R.M.
 TITLE Transgenic non-human animals for producing heterologous antibodies
 JOURNAL Patent: US 5789650-A 32 04-AUG-1998;
 FEATURES Location/Qualifiers
 source 1..42
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATTC 18
 |||||
 Db 11 CACTCCCATTC 1

RESULT 45
 LOCUS AR042946 42 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 32 from patent US 5814318.
 ACCESSION AR042946
 VERSION AR042946.1 GI:5963954

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 42)
 AUTHORS Lonberg, N. and Kay, R.M.
 TITLE Transgenic non-human animals for producing heterologous antibodies
 JOURNAL Patent: US 5814318-A 32 29-SEP-1998;
 FEATURES Location/Qualifiers
 source 1..42
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 5.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CACTCCCATTC 18
 |||||
 Db 11 CACTCCCATTC 1

Search completed: September 14, 2005, 11:03:30
 Job time : 2625 secs

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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 06:00:04 ; Search time 373 Seconds
(without alignments)
317.412 Million cell updates/sec

Title: US-10-643-801A-35

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 segs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4427878

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2002as:*
6: geneseqn2003as:*
7: geneseqn2003bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	65.0	54	2	AAV76917
C 2	13	65.0	60	6	ABN45267
C 3	12	60.0	12	5	ABH69241
C 4	12	60.0	12	5	ABH67956
C 5	12	60.0	20	6	AB193675
C 6	12	60.0	20	12	ADN31408
C 7	12	60.0	20	12	ADN31409
C 8	12	60.0	20	12	ADN31527
C 9	12	60.0	21	2	AAZ26938
C 10	12	60.0	22	13	ADN31699
C 11	12	60.0	24	6	AB183921
C 12	12	60.0	24	6	AB183920
C 13	12	60.0	26	6	ABG59154
C 14	12	60.0	26	6	ABQ88545
C 15	12	60.0	26	10	AD104496
C 16	12	60.0	29	2	AAV44981
C 17	12	60.0	29	2	AAV08886
C 18	12	60.0	39	2	AAZ28769
C 19	12	60.0	41	10	AA155696
C 20	12	60.0	51	4	AA175760

C 21	12	60.0	51	4	AA175759
C 22	12	60.0	51	4	AA175758
C 23	12	60.0	51	4	AAH38540
C 24	12	60.0	51	5	AB100487
C 25	12	60.0	60	6	ABN44520
C 26	12	60.0	60	6	ABN42321
C 27	11	55.0	13	5	ABF27951
C 28	11	55.0	13	5	ABF27950
C 29	11	55.0	13	5	ABF27950
C 30	11	55.0	13	5	ABF27950
C 31	11	55.0	17	2	AAV95069
C 32	11	55.0	18	8	ABA95013
C 33	11	55.0	18	8	ABA95013
C 34	11	55.0	18	8	ABA95013
C 35	11	55.0	19	2	AAV18643
C 36	11	55.0	20	2	AAV80303
C 37	11	55.0	20	3	AAV92200
C 38	11	55.0	20	9	ADA74107
C 39	11	55.0	20	9	ADA74107
C 40	11	55.0	20	12	AD157250
C 41	11	55.0	20	12	ADK96200
C 42	11	55.0	20	12	ADN31407
C 43	11	55.0	20	12	ADN89393
C 44	11	55.0	21	2	AAQ76368
C 45	11	55.0	21	4	AAA91279

ALIGNMENTS

RESULT 1
AAV76917/c
ID AAV76917 standard; DNA; 54 BP.
XX
AC AAV76917;
XX
DT 16-MAR-1999 (first entry)
XX
DE Staphylococcus aureus contig SEQ ID #2606.
XX
KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome; ds.
XX
OS Staphylococcus aureus.
XX
PN EP786519-A2.
XX
PD 30-JUL-1997.
XX
PF 07-JAN-1997; 97BP-00100117.
XX
PR 05-JAN-1996; 96US-0009661P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX
DR WPI; 1997-374922/35.
XX
PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S. aureus vaccines.
XX
PS Claim 1; Page 2287; 3271P; English.
XX
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S. aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or

CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against *S. aureus* infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC *S. aureus* in a sample. *S. aureus* is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the *S. aureus* DNA sequences contained on the computer
 CC readable medium

XX
 SQ Sequence 54 BP; 18 A; 4 C; 18 G; 14 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 2; Length 54;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TTGGCACTCCCAT 16
 Db 47 TTGGCACTCCCAT 35

RESULT 2

ABN45267
 ID ABN45267 standard; DNA; 60 BP.

XX
 AC ABN45267;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:18015.

KM Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-1B001903.

PR 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.

PS Example 1; SEQ ID NO 18015; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC oligonucleotide units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridizing selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 60 BP; 12 A; 14 C; 15 G; 19 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 6; Length 60;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TTGGCACTCCCAT 16
 Db 4 TTGGCACTCCCAT 16

RESULT 3

ABH69241/c

XX ID ABH69241 standard; DNA; 12 BP.

XX
 AC ABH69241;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 269218 for detecting SNP TSC0001665.

KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-1B000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piegenbrock C, Berlin K;

DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 269218; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABH00010-ABH99989, ABH00010-ABH99989 and ABH00010-ABH2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATCTT 19
DB 12 CACTCCCATCTT 1

RESULT 4
ABH67956
ID ABH67956 standard; DNA; 12 BP.
XX
XX
AC ABH67956;
XX

DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide primer SEQ ID NO 267933 for detecting SNP TSC0000710.
XX

XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

XX Homo sapiens.
XX
XX MO200177384-A2.
XX

PD 18-OCT-2001.
XX

PF 06-APR-2001; 2001MO-1B000713.
XX

PR 07-APR-2000; 2000DB-01019173.
XX

XX (EPIC-) EPIGENOMICS AG.
XX

PI Olek A, Piepenbrock C, Berlin K;
XX

DR WPI; 2001-657177/75.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX

PS Claim 1; SEQ ID NO 267933; 29pp + Sequence Listing; German.
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

XX Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
SQ

Query Match 60.0%; Score 12; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATTC 18
DB 1 CCACTCCCATTC 12

RESULT 5
ABI93675/c
ID ABI93675 standard; DNA; 20 BP.

XX ABI93675;
AC

DT 16-FEB-2002 (first entry)
XX

DE Capture oligonucleotide Zip ID#762 oligo #9.
XX

KM Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KM oncogene; tumour suppressor; human papillomavirus; forensic;
KM environmental monitoring; food industry; feed industry; ss.
XX

XX Synthetic.
XX

XX MO200179548-A2.
XX

PD 25-OCT-2001.
XX

PF 04-APR-2001; 2001MO-US010958.
XX

PR 14-APR-2000; 2000US-0197271P.
XX

PA (CORR) CORNELL RES FOUND INC.
XX

PI Barany F, Zirvi M, Gerry NP, Favis R, Kilman R;
XX

DR WPI; 2002-034366/04.
XX

PT Designing capture oligonucleotide probes for use on a support to which
complementary oligonucleotides hybridize with little mismatch.
XX

PS Example 5; Fig 29; 300pp; English.
XX

CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying (using a computer) identified ligation to a
CC beads occurred or absence of the target nucleotide sequences. ABI82074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX

XX Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
SQ

Query Match 60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
DB 15 GCATTGCCACTC 4

RESULT 6
ADN31408
ID ADN31408 standard; DNA; 20 BP.

```

XX AC ADN31408;
XX AD 12-AUG-2004 (first entry)
XX DT
XX DE Human forkhead box C2 antisense oligonucleotide ISIS227188.
XX
XX KW Human; ss; antisense; forkhead box C2; developmental disorder;
XX LM lymphedema; lymphedema-distichiasis; dysgenesis; iridocorneal angle;
XX KM Axenfeld-Rieger anomaly; congenital glaucoma.
XX
XX OS Homo sapiens.
XX
XX FH Key
XX FT modified_base
XX FT 1..20
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone and all cytidines are 5
XX FT -methylcytidines"
XX FT modified_base
XX FT 1..5
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residue"
XX FT modified_base
XX FT 16..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residue"
XX
XX PN US2004102621-A1.
XX
XX PD 27-MAY-2004.
XX
XX PF 21-NOV-2002; 2002US-00303635.
XX
XX PR 21-NOV-2002; 2002US-00303635.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Double KW;
XX
XX DR WPI; 2004-399740/37.
XX
XX PT New compound targeted to a nucleic acid molecule encoding forkhead box
XX C2, useful in diagnosing and treating developmental disorder.
XX
XX PS Example 15; SEQ ID NO 73; 80pp; English.
XX
XX CC The invention relates to a new compound 8-80 nucleobases in length (an
XX CC antisense oligonucleotide) targeted to a nucleic acid molecule encoding
XX CC forkhead box C2, where the compound specifically hybridizes with the
XX CC nucleic acid molecule encoding human forkhead box C2 appearing as
XX CC ADN31339 and inhibits the expression of forkhead box C2. Also included
XX CC are inhibiting the expression of forkhead box C2 in cells or tissues,
XX CC screening for a modulator of forkhead box C2, a diagnostic method for
XX CC identifying a disease state, a kit or assay device comprising the
XX CC compound and treating an animal having a disease or condition associated
XX CC with forkhead box C2. The compound and methods are useful in diagnosing
XX CC and treating developmental disorders e.g. lymphedemas such as lymphedema-
XX CC distichiasis, dysgenesis of the mouse iridocorneal angle similar to those
XX CC seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The
XX CC present sequence is an antisense oligonucleotide targeting forkhead box
XX C2.
XX
XX SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 12; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCATTGCCACTC 12
XX |||||
XX Db 6 GCATTGCCACTC 17

```

```

RESULT 7
ADN31409
ID ADN31409 standard; DNA; 20 BP.
XX
XX AC ADN31409;
XX
XX DT 12-AUG-2004 (first entry)
XX DE Human forkhead box C2 antisense oligonucleotide ISIS227189.
XX
XX KW Human; ss; antisense; forkhead box C2; developmental disorder;
XX LM lymphedema; lymphedema-distichiasis; dysgenesis; iridocorneal angle;
XX KM Axenfeld-Rieger anomaly; congenital glaucoma.
XX
XX OS Homo sapiens.
XX
XX FH Key
XX FT modified_base
XX FT 1..20
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone and all cytidines are 5
XX FT -methylcytidines"
XX FT modified_base
XX FT 1..5
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residue"
XX FT modified_base
XX FT 16..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residue"
XX
XX PN US2004102621-A1.
XX
XX PD 27-MAY-2004.
XX
XX PF 21-NOV-2002; 2002US-00303635.
XX
XX PR 21-NOV-2002; 2002US-00303635.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Double KW;
XX
XX DR WPI; 2004-399740/37.
XX
XX PT New compound targeted to a nucleic acid molecule encoding forkhead box
XX C2, useful in diagnosing and treating developmental disorder.
XX
XX PS Example 15; SEQ ID NO 74; 80pp; English.
XX
XX CC The invention relates to a new compound 8-80 nucleobases in length (an
XX CC antisense oligonucleotide) targeted to a nucleic acid molecule encoding
XX CC forkhead box C2, where the compound specifically hybridizes with the
XX CC nucleic acid molecule encoding human forkhead box C2 appearing as
XX CC ADN31339 and inhibits the expression of forkhead box C2. Also included
XX CC are inhibiting the expression of forkhead box C2 in cells or tissues,
XX CC screening for a modulator of forkhead box C2, a diagnostic method for
XX CC identifying a disease state, a kit or assay device comprising the
XX CC compound and treating an animal having a disease or condition associated
XX CC with forkhead box C2. The compound and methods are useful in diagnosing
XX CC and treating developmental disorders e.g. lymphedemas such as lymphedema-
XX CC distichiasis, dysgenesis of the mouse iridocorneal angle similar to those
XX CC seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The
XX CC present sequence is an antisense oligonucleotide targeting forkhead box
XX C2.
XX
XX SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 12; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY 1 GCATTGCCACTC 12
DB 9 GCATTGCCACTC 20

RESULT 8
ADN31527/c
ID ADN31527 standard; cDNA; 20 BP.

ADN31527;

12-AUG-2004 (first entry)

Human forkhead box C2 cDNA AS target region #25.

Human; ss; antisense; forkhead box C2; developmental disorder;
lymphoedema; lymphoedema-distichiasis; dysgenesis; iridocorneal angle;
Axenfeld-Rieger anomaly; congenital glaucoma.

Homo sapiens.

US2004102621-A1.

27-MAY-2004.

21-NOV-2002; 2002US-00303635.

21-NOV-2002; 2002US-00303635.

(ISIS-) ISIS PHARM INC.

Doble KW;

WPI; 2004-399740/37.

New compound targeted to a nucleic acid molecule encoding forkhead box C2, useful in diagnosing and treating developmental disorder.

Example 16; SEQ ID NO 192; 80bp; English.

The invention relates to a new compound 8-80 nucleobases in length (an antisense oligonucleotide) targeted to a nucleic acid molecule encoding forkhead box C2, where the compound specifically hybridises with the nucleic acid molecule encoding human forkhead box C2 appearing as AN31339 and inhibits the expression of forkhead box C2. Also included are inhibiting the expression of forkhead box C2 in cells or tissues, screening for a modulator of forkhead box C2, a diagnostic method for identifying a disease state, a kit or assay device comprising the compound and treating an animal having a disease or condition associated with forkhead box C2. The compound and methods are useful in diagnosing CC and treating developmental disorders e.g. lymphoedemas such as lymphoedema-distichiasis, dysgenesis of the mouse iridocorneal angle similar to those seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The present sequence is a forkhead box C2 nucleic acid region targeted by the antisense oligonucleotides.

Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
DB 15 GCATTGCCACTC 4

RESULT 9
AA226938
ID AA226938 standard; DNA; 21 BP.

AA226938;

DT 18-NOV-1999 (first entry)

Human chromosome 11 linked CHD1 gene mutation screening PCR primer #76.

Human; coronary heart disease susceptibility gene; CHD1; mutation;
chromosome 11; diagnosis; screening; PCR primer; metabolic disorder;
detection; hypolipidoproteinaemia; familial combined hyperlipidaemia;
insulin resistant syndrome X; multiple metabolic disorder; obesity;
diabetes; dyslipidaemic hypertension; ss.

Synthetic.

Homo sapiens.

WO945112-A2.

10-SEP-1999.

04-MAR-1999; 99WO-US004682.

04-MAR-1998; 98US-00034941.

06-APR-1998; 98US-0080934P.

(MYRI-) MYRIAD GENETICS INC.

Ballinger DG, Ding W, Wagner S, Hess MA;

WPI; 1999-540844/45.

New isolated coronary heart disease susceptibility gene, used to develop products for diagnosis and treatment of coronary heart disease and metabolic disorders.

Example 6; Page 98; 297bp; English.

The present invention describes the human chromosome 11-linked coronary heart disease susceptibility gene (CHD1). Mutations in the CHD1 locus in the germline are indicative of a predisposition to coronary heart disease or to metabolic disorders related to lipid metabolism. Products from the present invention can be used in the diagnosis of predisposition to coronary heart disease and to metabolic disorders, including hypolipidoproteinaemia, familial combined hyperlipidaemia, insulin resistant syndrome X or multiple metabolic disorder, obesity, diabetes and dyslipidaemic hypertension. CHD1 proteins can be used for treating coronary heart disease and metabolic disorders. The products can also be used for detection and drug screening. AA226932 to AA226841 and AA227027 to AA227029 represent human CHD1 nucleotide sequences. AA227027 to AA227029 represent human CHD1 proteins and protein sequences used in the exemplification of the present invention. AA226842 to AA226862 represent primers used in the identification of human CHD1; AA226863 to AA227014 represent PCR primers used in the screening of mutations in human CHD1; AA227015 to AA227026 represent oligonucleotides used in the exemplification of the present invention

Sequence 21 BP; 6 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCCA 15
DB 2 TTGGCACTCCCA 13

RESULT 10
ADS31699/c
ID ADS31699 standard; DNA; 22 BP.

ADS31699;

02-DEC-2004 (first entry)

Gene expression inhibition method erbB2 gene PCR primer #10.

```
XX
KM cyostatic: gene promoter methylation inducer; cell growth inhibitor;
KM erbB2 gene expression inhibitor; DNA methylation inducer; dsRNA; CpG;
KM human; gene expression; erbB2; tumour; gene transcription; promoter;
KM small interfering RNA; siRNA; gene silencing; ss; primer.
OS
XX Homo sapiens.
XX Synthetic.
XX WO2004076663-A1.
XX
XX 10-SEP-2004.
XX
XX 27-FEB-2004; 2004WO-JP002448.
XX
XX 27-FEB-2003; 2003US-0449860P.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
XX Taira K, Kawasaki H;
XX
XX WPI; 2004-662014/64.
XX
XX
XX Novel DNA methylation inducer containing double-stranded RNA targeting
XX region having CpG on DNA in mammalian cell, useful in suppressing gene
XX expression, and as cell growth inhibitor.
XX
XX
XX Example 4; SEQ ID NO 60; 98bp; Japanese.
XX
XX
XX The invention relates to a DNA methylation inducer (I) containing double-
XX stranded (ds)RNA that targets the region which contains CpG or CpNG (N is
XX A, T, C or G) on DNA in mammalian cell, or expression vector (VI) having
XX DNA that codes dsRNA that targets the region which contains CpG or CpNG
XX on DNA in mammalian cell. (I) is useful in the DNA methylation process,
XX which involves introducing (I) in a mammalian cell, where the mammalian
XX cell is obtained from human. (I) is useful as gene expression inhibitor
XX or cell growth inhibitor. A gene expression inhibitor (II) is useful for
XX suppressing gene expression, where the gene is a disease related gene.
XX The gene is erbB2 and the disease is the tumour. (I) is useful for
XX relevant to a disease, and the expression of the gene causes the disease.
XX controlling various biological activities in a mammal by controlling the
XX transcription level of the respective gene by methylating the respective
XX DNA. (I) or (II) enables specific methylation of the CpG island.
XX containing domain on a gene promoter of the target gene, where the
XX methylation of a promoter suppresses the expression of the target gene.
XX (I) induces sequence specific DNA methylation in a plant, and controls
XX the expression of the specific gene at the transcription level. (I)
XX enables DNA methylation in the promoter region of a gene, where the
XX methylation changes the structure of the DNA, enabling suppression of the
XX gene expression at the transcription level (DNA to mRNA). This sequence
XX corresponds to an erbB2 gene PCR primer used in the method to silence
XX gene expression in cells.
XX
XX
XX Sequence 22 BP; 4 A; 7 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX
XX Query Match 60.0%; Score 12; DB 13; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 4 TTGGCAGCTCCCA 15
XX 13 TTGGCAGCTCCCA 2
XX
XX
XX RESULT 11
XX AB183921
XX ID AB183921 standard; DNA; 24 BP.
XX
XX
XX AC AB183921;
XX
XX
XX 15-FEB-2002 (first entry)
XX
XX
XX Capture oligonucleotide zip ID#762 oligo #2.
XX
XX
```

```
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
XX
XX
XX Synthetic.
XX
XX WO200179548-A2.
XX
XX
XX 25-OCT-2001.
XX
XX
XX 04-APR-2001; 2001WO-US010958.
XX
XX
XX 14-APR-2000; 2000US-0197271P.
XX
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX
XX Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
XX WPI; 2002-034366/04.
XX
XX
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.
XX
XX
XX Example 5; Fig 25; 300bp; English.
XX
XX
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridise with little mismatch, where
XX (I) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX Epstein-Barr virus and polio virus, and parasitic infectious agents
XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX medineis. The method is also useful for detecting genetic diseases such
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX involved in DNA amplification, replication, recombination or repair, the
XX cancer is specifically associated with a gene selected from BRCA1 gene,
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX method is also used for environmental monitoring, forensics and the food
XX and feed industry, detecting complement scanning (using e.g. a scanning
XX electron microscope and infrared microscope) the support at the
XX particular sites and identifying if ligation of the oligonucleotide probe
XX sets occurred and correlating (using a computer) identified ligation to a
XX presence or absence of the target nucleotide sequences. AB182074 to
XX CC AB197546 represent oligonucleotide sequences used in the exemplification
XX of the present invention
XX
XX
XX Sequence 24 BP; 5 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX
XX Query Match 60.0%; Score 12; DB 6; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 GCATTGCCACTC 12
XX 6 GCATTGCCACTC 17
XX
XX
XX RESULT 12
XX AB183920/c
XX ID AB183920 standard; DNA; 24 BP.
XX
XX
XX AC AB183920;
XX
XX
XX 15-FEB-2002 (first entry)
XX
XX
XX Capture oligonucleotide zip ID#762 oligo #1.
XX
XX
```

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 PD
 PD 25-OCT-2001.
 PF 04-APR-2001; 2001WO-US010958.
 PF 14-APR-2000; 2000US-0197271P.
 PR (CORR) CORNELL RES FOUND INC.
 PA Barany F, Zivri M, Gerry NP, Favis R, Kliman R;
 PI WPI; 2002-034366/04.
 DR
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch.
 XX Example 5; Fig 25; 300pp; English.
 PS The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenzae, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC mediasi. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB19746 represent oligonucleotide sequences used in the exemplification
 CC of the present invention
 CC
 XX
 SQ Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCATTGCCACTC 12
 Db 19 GCATTGCCACTC 8
 RESULT 13
 ABSS9154 ID ABSS9154 standard; DNA; 26 BP.
 XX
 XX ABSS9154;
 AC
 XX 05-NOV-2002 (first entry)
 DT
 XX Human G-protein coupled receptor, probe #101.

XX Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;
 KW diabetes; cell signal processing; metabolic pathway modulation; cancer;
 KW adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;
 KW immune response; neurodegenerative disorder; inflammatory disorder;
 KW Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;
 KW probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200259313-A2.
 PD
 PD 01-AUG-2002.
 PF 18-DEC-2001; 2001WO-US049394.
 PF 18-DEC-2000; 2000US-0256635P.
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-0259743P.
 PR 10-JAN-2001; 2001US-0260718P.
 PR 12-JAN-2001; 2001US-0261498P.
 PR 24-JAN-2001; 2001US-0263689P.
 PR 08-FEB-2001; 2001US-0267464P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-0278150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-0285718P.
 PR 19-JUN-2001; 2001US-0299327P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Szytek KA;
 PI Giesman SJ, Vermet CAM, Shenoy SG, Gusev V, Malyanekar UM, Edinger S;
 PI Gerlach V, Smithson G, Store DJ, Sciore P, Macdougall JR, Gunther B;
 PI Peyman JA, Ellerman K, Gangolli BA, Millet I;
 XX WPI; 2002-599789/64.
 DR
 PT New G protein coupled receptor polypeptides and polynucleotides, useful
 PT in gene therapy, particularly for treating or preventing cardiomyopathy,
 PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
 PT in humans.
 XX
 PS Claim 9; Page 568; 685pp; English.
 CC The invention relates to novel isolated G-protein coupled receptor (GPCR)
 CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
 CC and antibody are useful for treating, preventing or alleviating a GPCR-
 CC associated disorder or a pathological state in a subject, particularly a
 CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
 CC diabetes, or a disorder related to cell signal processing and metabolic
 CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
 CC for diagnosing the presence or of predisposition to a disease associated
 CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
 CC and polypeptide are especially useful in therapeutic or prophylactic
 CC applications for disorders associated with aberrant GPCR expression or
 CC activity. The DNA encoding the protein is useful in gene therapy for
 CC treating the above conditions. Furthermore, the nucleic acids and
 CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
 CC cancer, uterus cancer, immune response, neurodegenerative disorders,
 CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
 CC Albright hereditary osteodystrophy. These are also useful in developing a
 CC powerful assay system for functional analysis of various human disorders,
 CC as well as in diagnostic applications. ABSS8747-ABSS9231 represent human
 CC GPCR coding sequences, primers and probes of the invention
 CC
 XX
 SQ Sequence 26 BP; 7 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCCA 15
 Db 5 TTGGCACTCCCA 16

RESULT 14
 AB088545 standard; DNA; 26 BP.

XX
 AC AB088545;
 DT 23-SEP-2002 (first entry)
 XX

Human GPCR probe SEQ ID NO:257.

XX
 DE Human GPCR probe SEQ ID NO:257.
 XX

KW Human; G protein coupled receptor; GPCR; GPCR; neuroprotective;
 KW nootropic; anti-HIV; antidiabetic; antidiabetic; anorectic; haemostatic;
 KW immunomodulator; anti-inflammatory; antidiabetic; anorectic; haemostatic;
 KW antibacterial; fungicide; protozoal; virucide; nephrotoxic; osteopathic;
 KW cardiant; antitumor; antidiabetic; hepatotropic; antiparkinsonian; HIV;
 KW vaccine; gene therapy; cell signal processing; cardiomypathy; diabetes;
 KW metabolic pathway modulation; atherosclerosis; cancer; obesity; asthma;
 KW infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer;
 KW allergy; cirrhosis; glomerulonephritis; stroke; haematopoietic disorder;
 KW systemic lupus erythematosus; probe; ss.

XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 PN WO200250276-A2.
 XX
 PD 27-JUN-2002.
 XX

PF 18-DEC-2001; 2001MO-US049347.
 XX

PR 18-DEC-2000; 2000US-0256635P.
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-0259743P.
 PR 10-JAN-2001; 2001US-0260718P.
 PR 12-JAN-2001; 2001US-0261988P.
 PR 24-JAN-2001; 2001US-0263899P.
 PR 08-FEB-2001; 2001US-0267464P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-0278150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-0285718P.
 PR 19-JUN-2001; 2001US-0299327P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX

PA (CURA-) CURAGEN CORP.
 XX

PI Li L., Padigar M., Ballinger R., Kekuda R., Colman S.D., Sciore P.,
 PI Smithson G., Payman J.A., Macdougall J.R., Vernet C.M., Shenoy S.,
 PI Gunther E., Millec I., Tchenev V.T., Anderson D., Gusev V., Malankar U.M.,
 PI Zhong H., Ellemann K.E., Wolenc A.;
 XX

XX
 DR WPI; 2002-557660/59.
 XX

PT New isolated human G-protein coupled receptor X (GPCR) polypeptide,
 PT useful for treating or preventing GPCR-associated disorders e.g.
 PT diabetes, atherosclerosis, cancer or obesity.
 PT

XX
 PS Example 3; Page 245; 354pp; English.
 XX

CC AB088354 to AB088417 represent human G protein coupled receptor (GPCR)
 CC CDNA sequences, and ABP51560 to ABP51624 represent human GPCR proteins
 CC from the present invention. GPCR sequences can have neuroprotective,
 CC nootropic, anti-HIV, antidiabetic, antidiabetic, cytoostatic,
 CC immunomodulator, anti-inflammatory, antidiabetic, anorectic, haemostatic,
 CC antibacterial, fungicide, protozoal, virucide, nephrotoxic, osteopathic,
 CC cardiant, antitumor, antidiabetic, hepatotropic and antiparkinsonian

CC activities, and can be used in vaccines and gene therapy. GPCR proteins,
 CC nucleic acid molecules, and antibodies from the present invention can be
 CC used for manufacturing a medicament for treating or preventing a GPCR-
 CC associated disorder or syndrome related to cell signal processing and
 CC metabolic pathway modulation, such as cardiomypathy, atherosclerosis,
 CC diabetes, cancer, obesity, infections (bacterial, fungal, protozoal or
 CC viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease,
 CC ulcers, allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus
 CC erythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be
 CC used diagnostically to monitor protein levels in tissues as part of a
 CC clinical testing procedure such as in determining the efficacy of a given
 CC treatment regimen. AB088418 to AB088639 represent PCR primers and probes
 CC for the human GPCRs of the present invention
 XX

SQ Sequence 26 BP; 7 A; 8 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred.No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGCACTCCCA 15
 Db 5 TTGGCACTCCCA 16

RESULT 15
 AD104496
 ID AD104496 standard; DNA; 26 BP.
 XX
 AC AD104496;
 XX
 DT 22-APR-2004 (first entry)
 XX

DE Human G-protein coupled receptor forward primer #43.

XX

KW ss; primer; PCR; human; G-protein coupled receptor; GPCR; cancer;
 KW breast; ovarian cancer; hypercalcaemia; endometriosis; Crohn's disease;
 KW appendicitis; cirrhosis; infertility; cardiovascular disorder;
 KW cardiomypathy; atherosclerosis; autoimmune disease; scleroderma;
 KW systemic lupus erythematosus; diabetes; pancreatitis;
 KW Alzheimer's disease; stroke; myasthenia gravis; schizophrenia;
 KW renal disorder; glomerulonephritis; renal tubular acidosis; immunogen;
 KW vaccine.

XX
 OS Homo sapiens.
 OS
 XX
 PN US2003198955-A1.
 XX
 PD 23-OCT-2003.
 XX

PF 19-DEC-2001; 2001US-00025806.
 XX

PR 18-DEC-2000; 2000US-0256635P.
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-0259743P.
 PR 10-JAN-2001; 2001US-0260718P.
 PR 12-JAN-2001; 2001US-0261988P.
 PR 24-JAN-2001; 2001US-0263899P.
 PR 08-FEB-2001; 2001US-0267464P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-0278150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-0285718P.
 PR 19-JUN-2001; 2001US-0299327P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX

PA (LIL/) LI L.
 PA (PADI/) PADIGAR M.
 PA (BALI/) BALLINGER R. A.
 PA (KEKU/) KEKUDA R.
 PA (COLM/) COLMAN S. D.
 PA (SPYT/) SPYTEK K. A.

PA (CASM/) CASMAN S J.
 PA (EDIN/) EDINGER S R.
 PA (GERL/) GERLACH V.
 PA (SCIO/) SCIORE P.
 PA (SMIT/) SMITHSON G.
 PA (PEYM/) PEYMAN J A.
 PA (MACD/) MACDOUGALL J R.
 PA (STON/) STONE D J.
 PA (VERN/) VERNET C A M.
 PA (SHEN/) SHENOY S G.
 PA (GUNT/) GUNTHER E.
 PA (MILL/) MILLET I.
 PA (TCHE/) TCHERNEV V T.
 PA (ANDE/) ANDERSON D W.
 PA (GUSE/) GUSEV V Y.
 PA (MALY/) MALYANKAR U M.
 PA (ZHON/) ZHONG H.
 PA (ELLE/) ELLERMAN K.
 PA (WOLE/) WOLENC A R.
 XX
 PI L I, Padigaru M, Ballinger RA, Kekuda R, Colman SD, Spytek KA,
 PI Casman SJ, Edinger SR, Gerlach V, Sciore P, Smithson G, Peyman JA,
 PI Macdougall JR, Stone DJ, Vernet CM, Shenoy SG, Gunther E, Millet I,
 PI Tchervet V, Anderson DW, Gusev VY, Malynkar UM, Zhong H;
 PI Ellerman K, Wolenc AR;
 XX
 DR WPI; 2003-852781/79.
 XX
 PT New isolated GPCRX polypeptide, useful for determining the predisposition
 PT to or presence of GPCRX-associated disorders or conditions, and in
 PT manufacturing a medicament for treating or preventing diseases such as
 PT cancer and diabetes.
 XX
 PS Example 3; SEQ ID NO 257; 221bp; English.
 XX
 CC The invention relates to an isolated G-protein coupled receptor (GPCRX)
 CC polypeptide. The polypeptide, nucleic acid, antibody, and their
 CC biologically active derivatives or fragments, are useful in determining
 CC the predisposition to or presence of GPCRX-associated disorders or
 CC syndromes and in manufacturing a medicament for treating, diagnosing or
 CC preventing the said disorders such as cancer (e.g. breast or ovarian
 CC cancers), hypercalcaemia, endometriosis, Crohn's disease, appendicitis,
 CC cirrhosis, infertility, cardiovascular disorders (e.g. cardiomyopathy,
 CC atherosclerosis), autoimmune diseases (e.g. scleroderma, systemic lupus
 CC erythematosus), diabetes, pancreatitis, Alzheimer's disease, stroke,
 CC myasthenia gravis, schizophrenia, renal disorders (e.g.
 CC glomerulonephritis, renal tubular acidosis), and/or other similar
 CC pathologies and disorders. The polypeptides are also useful as immunogens
 CC to produce antibodies and as vaccines. The present sequence represents a
 CC GPCR primer of the present invention.
 XX
 SQ Sequence 26 BP; 7 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 60.0%; Score 12; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 TTGCCACTCCCA 15
 DB 5 TTGCCACTCCCA 16
 XX
 RESULT 16
 AAV44981/C
 ID AAV44981 standard; cDNA; 29 BP.
 XX
 AC AAV44981;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE PCR primer for UCP2 gene transcriptional promoter sequence.
 XX
 KW Uncoupling protein 2; UCP2 gene; transcriptional promoter; mouse;

KW mitochondrial protein; cis transcriptional regulatory activity; therapy;
 KW expression modulator screening; fat feeding; diabetes; obesity;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5807740-A.
 PD 15-SEP-1998.
 XX
 PF 25-APR-1997; 97US-00846012.
 XX
 PR 25-APR-1997; 97US-00846012.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Chen J, Amaral MC;
 XX
 DR WPI; 1998-520130/44.
 XX
 PT Mouse UCP2 gene promoter - useful for forming transfected cell lines
 PT employed in drug screening assays.
 XX
 PS Example; Col 4; 9pp; English.
 XX
 CC This sequence is a PCR primer for the human mitochondrial uncoupling
 CC protein 2 (UCP2) gene transcriptional promoter of the invention. The
 CC promoter has cis transcriptional regulatory activity. Cells containing
 CC the promoter attached to a non-UCP2 gene, in which the non-UCP2 gene is a
 CC reporter gene can be used in screening assays for modulators of UCP2 gene
 CC expression, which may be useful for treating disorders in which the UCP2
 CC gene is upregulated in response to fat feeding, e.g. diabetes and obesity
 XX
 SQ Sequence 29 BP; 7 A; 5 C; 13 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 60.0%; Score 12; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 TTGCCACTCCCA 15
 DB 20 TTGCCACTCCCA 9
 XX
 RESULT 17
 AAV08886/C
 ID AAV08886 standard; cDNA; 29 BP.
 XX
 AC AAV08886;
 XX
 DT 20-MAR-2003 (revised)
 DT 25-FEB-1999 (first entry)
 XX
 DE PCR primer for UCP2 promoter.
 XX
 KW UCP2; promoter; transcription factor; modulator; diabetes; obesity;
 KW therapy; PCR primer; ds.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5849514-A.
 PD 15-DEC-1998.
 XX
 PF 19-JUN-1998; 98US-00100297.
 XX
 PR 25-APR-1997; 97US-00846012.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Chen J, Amaral MC;

XX
DR WPI; 1999-069722/06.
XX
PT Screening assay for modulators of UCP2 gene expression - based on
PT Intersection of transcription factor and defined UCP2 promoter sequence.
XX
PS Example; Col 4; 9pp; English.
XX
CC This sequence represents a PCR primer for the UCP2 promoter. The
CC amplified sequence is used in the method of the invention, which is a
CC screening assay for agents that modulate the effect of a transcription
CC factor on a UCP2 promoter comprising combining the promoter and
CC transcription factor in the presence and absence of a candidate agent and
CC determining any change in the effect of the transcription factor on the
CC promoter. The promoter comprises at least 50 nucleotides of a sequence
CC comprising nucleotides 1-460 of the UCP2 promoter (see AAV08879). The
CC method is used to identify agents that modulate UCP2 gene transcription
CC (agents that upregulate UCP2 are potentially useful for treating diabetes
CC and obesity). (Updated on 20-MAR-2003 to correct PF field.)
XX
SQ Sequence 29 BP; 7 A; 5 C; 13 G; 4 T; 0 U; 0 Other;
XX
Query Match 60.0%; Score 12; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4 TTGCCCACTCCCA 15
DB 20 TTGCCCACTCCCA 9
XX
RESULT 18
AAZ28769/c
ID AAZ28769 standard; DNA; 39 BP.
XX
AC AAZ28769;
XX
DT 01-FEB-2000 (first entry)
XX
DE G-less oligonucleotide GLESS7.
XX
KW Oligonucleotide; capture assay; tat; modulation; transcription; guanine;
KW mRNA expression; activator; inhibitor; detection; ss; gene expression;
KW antineoplastic; antifungal; antiviral; disease.
XX
OS Synthetic.
XX
XX W09950459-A2.
XX
PD 07-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US007127.
XX
PR 31-MAR-1998; 98US-00052995.
XX
PA (TULA-) TULARIK INC.
XX
PI Sivaraia M, Strulovici B, Flores OA;
PI WPI; 1999-610868/52.
XX
DR A new method for detecting RNA in a sample.
XX
PT Example I; Page 40; 60pp; English.
XX
PS The oligonucleotides AAZ28763-28772 are used in a capture assay for Tat-
CC modulated transcription of guanine (G)-less mRNA expression in vitro,
CC following addition of a potential transcriptional activator or inhibitor.
CC The method is used to detect a selected RNA in a sample, comprising: (a)
CC contacting a sample with an oligonucleotide comprising a region
CC complementary to the selected RNA to form an RNA/DNA duplex, (b) cleaving
CC single-stranded RNA in the sample, (c) binding RNA duplex to a
CC recognition reagent immobilized on a solid substrate, and (d) detecting

CC bound RNA duplex. The invention is used as a high throughput assay to
CC identify modulators of gene expression that may serve for example as
CC antineoplastic, antifungal or antiviral agents for the treatment of a
CC wide variety of diseases
XX
SQ Sequence 39 BP; 16 A; 0 C; 19 G; 4 T; 0 U; 0 Other;
XX
Query Match 60.0%; Score 12; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 8 CACTCCCATCTT 19
DB 27 CACTCCCATCTT 16
XX
RESULT 19
AAL55696/c
ID AAL55696 standard; DNA; 41 BP.
XX
AC AAL55696;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human zinc finger 32-56-related probe #1.
XX
KW Human; zinc finger 32.56; cancer; HIV; probe; ss.
XX
OS Homo sapiens.
XX
XX CN1381467-A.
XX
PD 27-NOV-2002.
XX
PF 18-APR-2001; 2001CN-00112608.
XX
PR 18-APR-2001; 2001CN-00112608.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
PI WPI; 2003-249003/25.
XX
DR New Polypeptide-human zinc finger protein-32.56, encoding polynucleotide,
PT antagonist and recombinant production, useful for treating cancer and
PT HIV.
XX
PS Example 7; Page 22; 0pp; Chinese.
XX
XX The invention relates to a novel human zinc finger 32.56 polypeptide, the
CC encoding polynucleotide, an antagonist and a method for recombinant
CC production. The polypeptide is useful for treating cancer and HIV
CC infection. The current sequence is that of the human zinc finger 32.56-
CC related probe #1
XX
SQ Sequence 41 BP; 10 A; 7 C; 10 G; 14 T; 0 U; 0 Other;
XX
Query Match 60.0%; Score 12; DB 10; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 9 ACTCCCATCTT 20
DB 27 ACTCCCATCTT 16
XX
RESULT 20
AAT17560/c
ID AAT17560 standard; DNA; 51 BP.
XX
AC AAT17560;
XX

PD 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US032758.
PF
XX 30-NOV-1999; 99US-0168138P.
PR
XX 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shimkels RA, Leach M;
PI
XX WPI; 2001-356160/37.
DR
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PS
XX Claim 1; Page 877; 2653pp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (1) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (1) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 13 A; 9 C; 16 G; 13 T; 0 U; 0 Other;
Query Match 60.0%; Score 12; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGCCACTGCCAT 16
DB 45 TGCCACTGCCAT 34
AAH38540
ID AAH38540 standard; DNA; 51 BP.
XX
AC AAH38540;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 1336.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polyarthritis; kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; ds.
OS
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.

XX
XX 15-OCT-1999; 99US-0160096P.
PR
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA
XX
XX Picoult-Newburg L, Pohl M;
PI
XX WPI; 2001-290930/30.
DR
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
PS
XX Claim 1; Page 56; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
XX DNA flanking the site of a single nucleotide polymorphism
XX
SQ Sequence 51 BP; 12 A; 16 C; 14 G; 9 T; 0 U; 0 Other;
Query Match 60.0%; Score 12; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGCCACTC 12
DB 28 GCATTGCCACTC 39
ABL00487/c
ID ABL00487 standard; DNA; 51 BP.
XX
AC ABL00487;
XX
XX 05-MAR-2002 (first entry)
XX
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:478.
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
XX immunosuppressive; antiinflammatory; neuroprotective; antitumor;
XX autoimmune disease; inflammation; cancer; nervous system disease;
XX infection; polymorphic protein; ds.
OS
XX Homo sapiens.
XX
XX WO200138586-A2.
XX
XX 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-US032311.
XX

PR 24-NOV-1999; 99US-0167383P.
 XX (CURA-) CURAGEN CORP.
 XX
 XX Shinketsu RA, Leach M;
 XX WPI; 2001-355949/37.
 DR
 XX Isolated human nucleic acids comprising one or more single nucleotide
 PT polymorphisms, useful for treating a subject suffering from a pathology,
 PT e.g. autoimmune diseases, ascribed to the presence of a sequence
 PT polymorphism.
 XX
 XX Claim 1; Page 392; 674pp; English.
 PS
 XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
 CC to ABB56903 represent human peptides encoded by some of the SNP
 CC oligonucleotides. The sequences from the present invention can have
 CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
 CC and antibodies from the present invention can be used for treating a
 CC subject suffering from, at risk for, or suspected of, suffering from a
 CC pathology ascribed to the presence of a sequence polymorphism. The
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs
 CC are also useful for determining which forms of a characterized
 CC polymorphism are present in individuals. The antibodies may be used in
 CC the detection, quantitation and/or cellular or tissue localisation of a
 CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
 CC protein within appropriate physiological samples)
 CC
 XX
 XX Sequence 51 BP; 12 A; 11 C; 15 G; 13 T; 0 U; 0 Other;
 SQ
 Query Match 60.0%; Score 12; DB 5; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCATTGCCACTC 12
 |||||
 Db 27 GCATTGCCACTC 16

RESULT 25
 ABN44520
 ID ABN44520 standard; DNA; 60 BP.
 XX
 AC ABN44520;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:17268.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-IB001903.
 XX
 PR 28-JUL-2000; 2000US-0221607P.
 PR 02-MAY-2001; 2001US-0287724P.
 XX
 XX (COMP-) COMPUGEN INC.
 PA
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX WPI; 2002-257383/30.
 XX

PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.
 XX
 XX Example 1; SEQ ID NO 17268; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridising selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABB27253 to ABB59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 XX Sequence 60 BP; 11 A; 17 C; 13 G; 19 T; 0 U; 0 Other;
 SQ
 Query Match 60.0%; Score 12; DB 6; Length 60;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCATTGCCACTC 12
 |||||
 Db 44 GCATTGCCACTC 55

RESULT 26
 ABN42321/c
 ID ABN42321 standard; DNA; 60 BP.
 XX
 AC ABN42321;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:15069.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-IB001903.
 XX
 PR 28-JUL-2000; 2000US-0221607P.
 PR 02-MAY-2001; 2001US-0287724P.
 XX
 XX (COMP-) COMPUGEN INC.
 PA
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX WPI; 2002-257383/30.
 XX
 XX New oligonucleotide libraries comprising oligonucleotides which

PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.

Example 1; SEQ ID NO 15069; 47bp; English.

CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 60 BP; 17 A; 11 C; 19 G; 13 T; 0 U; 0 Other;

Query Match Best Local Similarity 60.0%; Score 12; DB 6; Length 60;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTCCCATCTT 20
DB 17 ACTCCCATCTT 6

RESULT 27

ABF27951
ID ABF27951 standard; DNA; 13 BP.

AC ABR27951;

DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 127948 for detecting SNP TSC0032026.

KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX Claim 1; SEQ ID NO 127948; 29bp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;

Query Match Best Local Similarity 55.0%; Score 11; DB 5; Length 13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTCGCCATCTT 20
DB 3 CTCGCCATCTT 13

RESULT 28

ABF27950/C
ID ABF27950 standard; DNA; 13 BP.

AC ABR27950;

DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 127947 for detecting SNP TSC0032026.

KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 127947; 29bp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 CTCCTCATTTCT 20
 |||||
 DB 11 CTCCTCATTTCT 1

RESULT 29

ABCI4054/C
 ID ABCI4054 standard; DNA; 13 BP.

AC ABCI4054;

XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO-14061 for detecting SNP TSC0003215.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

PN 18-OCT-2001.

PD 06-APR-2001; 2001WO-IB000713.

PF 07-APR-2000; 2000DE-01019173.

PR (EPIG-) EPIGENOMICS AG.

PA Olek A, Piepenbrock C, Berlin K;

PI WPI; 2001-657177/75.

DR Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

PS Claim 1; SEQ ID NO 14061; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ACTGCCATTCT 19
 |||||
 DB 13 ACTGCCATTCT 3

RESULT 30

ABCI4055
 ID ABCI4055 standard; DNA; 13 BP.

AC ABCI4055;

XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 14062 for detecting SNP TSC0003215.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

PN 18-OCT-2001.

PD 06-APR-2001; 2001WO-IB000713.

PF 07-APR-2000; 2000DE-01019173.

PR (EPIG-) EPIGENOMICS AG.

PA Olek A, Piepenbrock C, Berlin K;

PI WPI; 2001-657177/75.

DR Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

PS Claim 1; SEQ ID NO 14062; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ACTGCCATTCT 19
 |||||
 DB 1 ACTGCCATTCT 11

RESULT 31

AAV95069
 ID AAV95069 standard; RNA; 17 BP.

AC AAV95069;

XX 24-FEB-1999 (first entry)

DE Canine IL-2 receptor g-chain substrate position 17.

XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;

KM hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
KM autoimmune disease; psoriasis; allergy; inflammatory disease;
KM graft rejection; ss.
XX
OS Synthetic.
OS Canis sp.
PN WO9824913-A2.
PD 11-JUN-1998.
XX
XX 02-DEC-1997; 97WO-US021748.
PR 03-DEC-1996; 96US-00758306.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PI Stinchcomb DT, Mcswigen JA;
XX WPI; 1998-33332/29.
DR
XX
XX
PT Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer,
PT autoimmune disease and allergies.
XX
XX Claim 4; Page 45; 61pp; English.
XX
CC The present sequence invention describes ribozymes targeted to modulate
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.
CC AA93889 to AA94574 represent specifically claimed ribozymes, and
CC AA94575 to AA95260 represent specifically claimed substrate sequences
CC from the present invention. The ribozymes can be used for the treatment
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
CC and other inflammatory conditions. The ribozymes are also used to induce
CC tolerance in a recipient to alloantigen from a donor
XX
SQ Sequence 17 BP; 4 A; 8 C; 2 G; 0 T; 3 U; 0 Other;
Query Match 55.0%; Score 11; DB 2; Length 17;
Best Local Similarity 72.7%; Pred. No. 1.2e+04;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 CATGCCACTC 12
Db 6 CAUUGCCACCTC 16
RESULT 32
ABA95013/c
ID ABA95013 standard; DNA; 18 BP.
XX
XX ABA95013;
AC
XX
DT 11-SEP-2003 (revised)
DT 21-MAY-2002 (first entry)
XX
XX ISAV structural protein-1 (SP-1) forward primer.
XX
XX Structural protein-1; SP-1; infectious salmon anaemia virus; ISAV;
KM infectious salmon anaemia; ISA; vaccine; vitruclide; fish; PCR primer; ss.
OS
XX Infectious salmon anemia virus.
XX
XX
PN EP1094069-A1.
PD 25-APR-2001.
XX
XX 12-OCT-2000; 2000EP-00203555.
PF
XX 18-OCT-1999; 99EP-00203401.
PR
XX (ALKU) AKZO NOBEL NV.
PA
XX Biering E, Krossoy B;
PI

XX
DR WPI; 2001-487577/29.
XX
XX
PT New polynucleotide encoding structural protein-1 of infectious salmon
PT anemia virus in vaccine preparation for protecting fish against the viral
PT infection, and in diagnostics.
XX
XX Disclosure; Page 5; 24pp; English.
XX
XX
XX The invention relates to a structural protein-1 (SP-1) of infectious
CC salmon anaemia virus (ISAV). The SP-1 polynucleotide, protein or specific
CC antibodies are useful in diagnostics, and in vaccines to protect fish
CC against infection with ISAV. The SP-1 polynucleotide is useful for
CC producing vector vaccines against the virus, and for recombinant
CC production of SP-1, substantially free from other ISA viral protein. The
CC present sequence represents an oligonucleotide derived from the ISAV SP-1
CC DNA, that can be used as a primer. (Updated on 11-SEP-2003 to standardise
CC OS field)
XX
SQ Sequence 18 BP; 3 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
Query Match 55.0%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGCCACTCCCA 15
Db 15 TGCCACTCCCA 5
RESULT 33
ABX93931/c
ID ABX93931 standard; DNA; 18 BP.
XX
AC ABX93931;
XX
DT 04-JUN-2003 (first entry)
XX
XX pCDNA3 vector polylinker PCR primer.
XX
XX
KM Human; androgen receptor; AR; cytosolic; androgen receptor inhibitor;
KM gene therapy; ribozyme; cell proliferation; prostatic cancer cell;
KM prostate hyperplasia; prostate cancer; androgen dependent pathology; ss;
KM hammerhead ribozyme; HR2; PCR; primer; polylinker; pCDNA3.
XX
OS Synthetic.
XX
XX US6489163-B1.
PN
XX
PD 03-DEC-2002.
XX
XX 08-MAY-1997; 97US-00853164.
PR
XX 08-MAY-1996; 96US-0016590P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX Roy AK, Chen S;
PI
XX WPI; 2003-352114/33.
DR
XX
XX
XX New synthetic ribozyme that cleaves androgen receptor mRNA, useful for
PT treating prostate hyperplasia or cancer, and other androgen dependent
PT pathologies.
XX
XX
PS Disclosure; Col 6; 38pp; English.
XX
XX The invention describes a synthetic ribozyme (I) that cleaves androgen
CC receptor mRNA. A vector comprising (I) is useful for reducing androgen
CC receptor activity in cultured prostate cells, by providing to the cells a
CC preparation comprising the vector. The vector is also useful for
CC inhibiting the proliferation of prostatic cancer cells in vitro, by
CC providing the vector expressing (I) to the cells. (I) is useful for

CC treating prostate hyperplasia or cancer, and other androgen dependent
 CC pathologies. This sequence represents a primer used to detect expression
 CC of hammerhead ribozyme HR2 in cultured cells
 XX
 XX
 SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TGGCACTCCCA 15
 DB 13 TGGCACTCCCA 3

RESULT 34

ADA61988/C
 ID ADA61988 standard; DNA; 18 BP.
 XX
 AC ADA61988;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Vector pCDNA3 RT-PCR primer.
 XX
 KM Cytostatic; ss; androgen receptor; ribozyme; prostatic hyperplasia;
 KM prostate cancer; PCR; primer; RT-PCR; reverse transcriptase PCR; pCDNA3.
 XX
 OS Synthetic.
 XX
 PN US2003077639-A1.
 XX
 PD 24-APR-2003.

XX 17-SEP-2002; 2002US-00246078.
 PF 08-MAY-1996; 96US-0016590P.
 PR 08-MAY-1997; 97US-00853164.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Roy AK, Chen S;
 PT WPI; 2003-615997/58.

PT New synthetic ribozyme capable of selectively targeting androgen receptor
 PT mRNA, useful in inactivating androgen receptor gene expression, and for
 PT treating prostate hyperplasia.
 XX
 XX
 PS Disclosure; Page 7; 40pp; English.

CC The invention relates to synthetic ribozyme capable of selectively
 CC targeting the androgen receptor mRNA. Also included are a gene encoding
 CC the synthetic ribozyme, a vector comprising the gene (where expression of
 CC the gene in a human prostatic cancer cell is capable of inhibiting
 CC androgen receptor activation), reducing androgen receptor activity in an
 CC animal having prostatic hyperplasia by administering a preparation
 CC comprising the vector, and treating prostatic hyperplasia by
 CC administering to the patient a formulation of an active preparation of a
 CC ribozyme gene construct comprising a human promoter sequence in a vector
 CC carrier (where the ribozyme gene construct comprises a ribozyme gene that
 CC provides an expression product capable of selectively reducing androgen
 CC receptor activation). The synthetic ribozyme is capable of selectively
 CC targeting androgen receptor mRNA and can be used in the inactivation of
 CC androgen receptor gene expression, and for treating prostatic hyperplasia
 CC and prostate cancer. The present sequence is reverse transcriptase (RT)-
 CC PCR primer used to assess ribozyme expression in transfected cells,
 CC designed against the vector pCDNA3.

Query Match 55.0%; Score 11; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TGGCACTCCCA 15
 DB 13 TGGCACTCCCA 3

RESULT 35
 AAV18643
 ID AAV18643 standard; DNA; 19 BP.

XX AAV18643;
 XX
 DT 21-JUL-1998 (first entry)
 XX
 DE Homo sapiens BAP-1 PCR primer.
 XX
 KM BRCAL associated; BAP-1; breast cancer; ovarian cancer;
 KM breast and ovarian cancer susceptibility gene; diagnosis;
 KM ubiquitin carboxy-terminal hydrolase; activity; ss.
 XX
 OS Synthetic.

XX
 PN W09805968-A1.
 XX
 PD 12-FEB-1998.
 XX
 PF 30-JUL-1997; 97WO-US013684.
 XX
 PR 02-AUG-1996; 96US-0022997P.
 PR 19-FEB-1997; 97US-0038109P.
 XX
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX
 PI Rauscher FJ, Jensen DE;
 XX
 DR WPI; 1998-145723/13.

XX DNA encoding mammalian BRCAL associated protein, BAP-1 - useful for, e.g.
 PT detecting cancer involving breast and ovarian cancer susceptibility gene
 PT BRCAL.
 XX
 PS Example 8; Page 45; 100pp; English.

XX The sequence is that of a PCR primer which was used in the mutational
 CC analysis of BAP-1 (BRCAL associated protein) cDNA
 CC
 XX Sequence 19 BP; 4 A; 10 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCAATT 17
 DB 6 CCACTCCCAATT 16

RESULT 36
 AAV80303/C
 ID AAV80303 standard; DNA; 20 BP.

XX AAV80303;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Murine GILR cDNA specific reverse primer.

XX Glucocorticoid-induced leucine-zipper family related protein; GILR;
 KM apoptosis; lymphocyte; recombinant; medicament; Fas-Ligand; AIDS;
 KM CD3/T cell receptor; TCR; intracellular mediator; treatment; tumour;
 KM inflammation; acute hepatitis; autoimmune disease; diabetes; mouse;
 KM multiple sclerosis; graft rejection; immunodeficiency; HIV; detection;

PF 24-JAN-2002; 2002US-00053662.
 XX
 PR 24-JAN-2002; 2002US-00053662.
 XX
 PA (BAIR/) BAIRD J.
 PA (LIND/) LINDER K.
 PA (MENE/) MENEGUZZI G.
 PA (SPIR/) SPIRITO F.
 PA (CHAR/) CHARLESWORTH A.
 XX
 PI Baird J, Linder K, Meneguzzi G, Spirito F, Charlesworth A;
 DR WPI; 2003-626651/59.
 XX
 PT New isolated equine laminin gamma 2 polypeptide and encoding
 PT polynucleotide, useful for diagnosing junctional epidermolysis bullosa in
 PT horses.
 PS
 PS Example 2; Page 5; 34pp; English.
 XX
 CC The invention relates to the equine laminin gamma-2 polypeptide and the
 CC polynucleotide encoding it. The invention also relates to a method for
 CC diagnosing junctional epidermolysis bullosa (JEB) in a horse, comprising
 CC obtaining a biological sample from the horse, isolating DNA and
 CC amplifying the DNA encoding laminin gamma-2 using appropriate primers and
 CC analysing the amplified nucleic acid to identify the presence of a
 CC mutation, where the homozygous presence of the mutated nucleic acid
 CC encoding laminin gamma-2 indicates the presence of epidermolysis bullosa.
 CC Alternatively, the protein component from the sample can be isolated and
 CC screened for laminin gamma-2, where the absence of laminin gamma-2
 CC polypeptide indicates the presence of JEB. The laminin gamma-2 nucleic
 CC acid, proteins and antibodies against the proteins are useful for
 CC diagnosing JEB in horses. This sequence represents a PCR primer used to
 CC amplify cDNA encoding equine laminin gamma-2.
 XX
 SQ Sequence 20 BP; 1 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
 XX
 QY Query Match 55.0%; Score 11; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 10 CTCGCATTCTT 20
 7 CTCGCATTCTT 17
 XX
 RESULT 39
 ADA24256
 ID ADA24256 standard; DNA; 20 BP.
 XX
 AC ADA24256;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Major allergenic storage protein FAGAG1 PCR primer FAG22 SEQ ID NO:9.
 XX
 KM food testing; allergen; PCR primer; Fagopyrum esculentum;
 KM major allergenic storage protein; FAGAG1; ss.
 XX
 OS Synthetic.
 OS Fagopyrum esculentum.
 XX
 PN WO2003068964-A1.
 XX
 PD 21-AUG-2003.
 PD
 PF 26-SEP-2002; 2002WO-JP009982.
 PF
 PR 15-FEB-2002; 2002JP-00038930.
 PR
 XX (NISS) NISSHIN SEIFUN GROUP INC.
 PA
 PT Yamakawa H, Suzuki E, Miyatake K, Hayakawa K;

XX
 DR WPI; 2003-637145/60.
 XX
 PT PCR-based method for testing foods using specific primers designed from
 PT genes of target substance, useful in detecting trace components or
 PT identifying specific harmful allergens in (processed) foods.
 PS
 PS Disclosure; Page 10; 38pp; Japanese.
 XX
 CC The present invention describes a method for testing the presence or
 CC absence of a specific substance in a food by performing PCR with primers
 CC which are designed on the basis of data obtained from a part of a gene of
 CC the specific substance. Also described: (1) a similar method for
 CC detecting a trace component contained in a food, or for identifying a
 CC harmful allergen specific to a consumer of such substance by performing
 CC PCR with primers which are designed on the basis of data obtained from a
 CC part of a gene of the specific substance; (2) primers for PCR applicable
 CC in food testing which are designed on the basis of data obtained from a
 CC part of a gene of the specific substance; and (3) kits for determining
 CC concentration of a specific substance in the food containing the primers.
 CC The methods are useful for testing foods, which can be used in detecting
 CC trace components or identifying specific harmful allergens in (processed)
 CC foods, particularly applicable in food safety and management. The present
 CC sequence represents a PCR primer for a Fagopyrum esculentum major
 CC allergenic storage protein designated FAGAG1, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 20 BP; 1 A; 11 C; 1 G; 7 T; 0 U; 0 Other;
 XX
 QY Query Match 55.0%; Score 11; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 10 CTCGCATTCTT 20
 9 CTCGCATTCTT 19
 XX
 RESULT 40
 ADI57250/c
 ID ADI57250 standard; DNA; 20 BP.
 XX
 AC ADI57250;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE ATP-binding cassette transporter ABCG2 SNP primer #7.
 XX
 KM drug transport capability; polymorphism; ABCG2; polymorphic mutation;
 KM drug sensitivity; anti-cancer drug; cancer therapy;
 KM cancer cell detection; indolocarbazole compound; human;
 KM ABC transporter superfamily;
 KM ATP-binding cassette transporter superfamily;
 KM single nucleotide polymorphism; SNP; PCR; primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO2003107249-A1.
 PN
 PD 24-DEC-2003.
 PD
 PF 13-JUN-2003; 2003WO-JP007534.
 PF
 PR 17-JUN-2002; 2002JP-00175806.
 PR
 XX (BANY) BANYU PHARM CO LTD.
 PA
 PI Kotani H, Mizunari S;
 PI
 DR WPI; 2004-156349/15.
 DR
 XX Predicting drug transport capability of mammalian cell by collecting
 PT sample from mammal, determining polymorphism of nucleotide sequence of

PT ABCG2 gene or polymorphism of amino acid sequence of ABCG2 polypeptide.
XX
PS Claim 13; SEQ ID NO 9; 76pp; English.
XX
CC The invention describes a method of predicting a drug transport
CC capability of a mammalian cell involving collecting a sample from a
CC mammal, determining a polymorphism of the nucleotide sequence of ABCG2
CC gene or a polymorphism of the amino acid sequence of ABCG2 polypeptide.
CC The method is useful for predicting drug transport capability of a
CC mammalian cell. Polynucleotides comprising single nucleotide
CC polymorphisms or polypeptides comprising polymorphic mutations of the
CC ABCG2 protein are useful as diagnostic agent for diagnosing drug
CC sensitivity which involves analyzing a biological sample from a subject
CC and determining the presence or absence of the polynucleotides or
CC polypeptides, where the subject having the polynucleotides or
CC polypeptide is suggested to be sensitive to the indolocarbazole compound.
CC A transformed cell comprising an ABCG2 protein mutant is useful for
CC measuring drug transport capability. By predicting drug transport
CC capability of a mammalian cell, sensitivity of a patient to various drugs
CC such as anti-cancer drugs can be diagnosed and an indicator for the
CC cancer therapy can be obtained. As a result of selecting an anti-cancer drug in
CC cancer therapy and, particularly, detecting a cancer cell(s) which is
CC selectively sensitive to indolocarbazole compounds, it is now possible to
CC dose of the indolocarbazole compounds for the therapy. In addition, the optimum
CC at the same time, side effect of the compounds is reduced whereby a
CC highly effective method of using the indolocarbazole compounds is
CC provided. This sequence represents a primer used to identify ans sequence
CC single nucleotide polymorphisms of the human ABC transporter superfamily
CC (ATP-binding cassette transporter superfamily) protein ABCG2.
CC
SQ Sequence 20 BP; 11 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 55.0%; Score 11; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 CTCCCATCTT 20
Db 18 CTCCCATCTT 8
RESULT 41
ADK96200/c
ID ADK96200 standard; DNA; 20 BP.
XX
AC ADK96200;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer of the invention #1920.
XX
KW human; single nucleotide polymorphism; SNP; ss; primer.
XX
OS Synthetic.
XX
PN JP2003259875-A.
XX
PD 16-SEP-2003.
XX
PF 08-MAR-2002; 2002JP-00064373.
XX
PR 08-MAR-2002; 2002JP-00064373.
XX
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX
DR WPI; 2004-093977/10.
XX
PT Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX
PS Claim 2; SEQ ID NO 5229; 2627pp; Japanese.

XX
CC The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 55.0%; Score 11; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 ATTGCCATCTC 13
Db 11 ATTGCCATCTC 1
RESULT 42
ADN31407
ID ADN31407 standard; DNA; 20 BP.
XX
AC ADN31407;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human forehead box C2 antisense oligonucleotide ISIS227187.
XX
KW Human; ss; antisense; forehead box C2; developmental disorder;
KW Lympeedema; lympeedema-dietrichiaels; dygenesis; iridocorneal angle;
KW Axenfeld-Rieger anomaly; congenital glaucoma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
XX
PN US2004102621-A1.
XX
PD 27-MAY-2004.
XX
PF 21-NOV-2002; 2002US-00303635.
XX
PR 21-NOV-2002; 2002US-00303635.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KM;
XX
DR WPI; 2004-399740/37.
XX
PT New compound targeted to a nucleic acid molecule encoding forehead box
PT C2, useful in diagnosing and treating developmental disorder.
XX
PS Example 15; SEQ ID NO 72; 80pp; English.
XX
CC The invention relates to a new compound 8-80 nucleobases in length (an
CC antisense oligonucleotide) targeted to a nucleic acid molecule encoding
CC forehead box C2, where the compound specifically hybridises with the
CC nucleic acid molecule encoding human forehead box C2 appearing as
CC ADN3139 and inhibits the expression of forehead box C2. Also included

CC are inhibiting the expression of forkhead box C2 in cells or tissues.
 CC screening for a modulator of forkhead box C2, a diagnostic method for
 CC identifying a disease state, a kit or assay device comprising the
 CC compound and treating an animal having a disease or condition associated
 CC with forkhead box C2. The compound and methods are useful in diagnosing
 CC and treating developmental disorders e.g. lymphedemas such as lymphoedema-
 CC distichiasis, dysgeneses of the mouse iridocorneal angle similar to those
 CC seen in human Axenfeld-Rieger anomaly and congenital glaucoma. The
 CC present sequence is an antisense oligonucleotide targeting forkhead box
 C2.

XX Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCATTC 12
 |||||
 DB 1 CATTGCCATTC 11

RESULT 43

ADN89393
 ID ADN89393 standard; DNA; 20 BP.

XX
 AC ADN89393;

XX 12-AUG-2004 (first entry)

DE Human CD24 antisense oligonucleotide #72.

XX ss; human; antisense therapy; CD24; hyperproliferative disorder; probe.

XX Homo sapiens.

OS Location/Qualifiers

XX Key

XX modified_base 1..20

XX /tag= b

XX /mod_base= Other

XX /note= "phosphorothioate backbone. All cytidines are 5-

XX modified_base 1..5

XX /tag= a

XX /mod_base= Other

XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX /tag= c

XX /mod_base= Other

XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX US2004097448-A1.

XX 20-MAY-2004.

XX 19-NOV-2002; 2002US-00300236.

XX 19-NOV-2002; 2002US-00300236.

XX (ISIS-) ISIS PHARM INC.

XX Watt AT;

XX WPI; 2004-389189/36.

CC antisense oligonucleotides are useful for treating a disease or condition
 CC associated with CD24, such as a hyperproliferative disorder. They are
 CC also useful in research and diagnostics for modulating the expression of
 CC CD24. The present sequence represents a human CD24 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCATTC 12
 |||||
 DB 1 CATTGCCATTC 11

RESULT 44

AAQ76368/C
 ID AAQ76368 standard; cDNA; 21 BP.

XX
 AC AAQ76368;

XX 25-MAR-2003 (revised)

XX 22-JUN-1995 (first entry)

XX Oligonucleotide DNA primer 7 to human IGE mRNA.

XX Epsilon CH4; IGE; immunoglobulin; diagnosis; therapy; hypersensitivity;

XX oligonucleotide; DNA primer; ss.

XX Synthetic.

XX WO9421676-A1.

XX 29-SEP-1994.

XX 24-MAR-1994; 94WO-US003243.

XX 24-MAR-1993; 93US-00037579.

XX (REGC) UNIV CALIFORNIA.

XX Saxon A, Zhang K, Max EB;

XX WPI; 1994-316938/39.

XX New IGE isoforms and nucleic acid sequences - are used to develop prods.

XX for diagnosis and treatment of IGE-mediated immune hypersensitivity

XX conditions.

XX Disclosure; Page 15; 45pp; English.

XX This primer was designed to detect human IGE (epsilon) mRNA containing

XX membrane exon sequences. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 21 BP; 6 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTGCCATTC 18
 |||||
 DB 11 CACTGCCATTC 1

RESULT 45

AAA91279/C
 ID AAA91279 standard; DNA; 21 BP.

XX
 AC AAA91279;

XX The invention relates to antisense oligonucleotides which are targeted

to, and inhibit the expression of, nucleic acid encoding human CD24. The

DT 06-AUG-2003 (revised)
 DT 08-MAY-2001 (first entry)
 XX
 DE GURAV-5 nucleotide sequence primer LR8-1F.
 XX
 KW GURAV-5; grapevine leafroll virus; GURAV infection; GURAV coat protein;
 KW GURAV HSP70 homologue protein; viral gene mapping; PCR primer;
 XX plant disease resistance; ss.
 OS Grapevine leafroll virus.
 XX
 XX MO200105957-A2.
 XX
 XX 25-JAN-2001.
 XX
 XX 19-JUL-2000; 2000MO-US019708.
 XX
 XX 19-JUL-1999; 99US-0144453P.
 XX
 PA (AGRI-) AGRITROPE INC.
 XX
 XX Good XC, Monis J;
 XX
 XX WPI; 2001-147339/15.
 XX
 XX
 PT Novel grapevine leafroll virus polynucleotide useful as diagnostic and
 PT probe, for viral gene mapping and for induced plant disease resistance.
 XX
 PS Example 3; Page 35; 60pp; English.
 XX
 CC This sequence represents a primer used to isolate the grapevine leafroll
 CC virus (GURAV-5) DNA sequence of the invention. The DNA sequence can be
 CC used in an expression construct. The construct is useful for providing
 CC resistance to GURAV infection in a recombinant plant cell by transforming
 CC the plant cell with it, where transcription of the polynucleotide
 CC sequence interferes with a normal viral function such as movement,
 CC encapsidation or replication of viral RNA. The polynucleotide sequence is
 CC expressed as an antisense sequence and encodes a GURAV coat protein,
 CC preferably a defective GURAV coat protein or a GURAV HSP70 homologue
 CC protein. The GURAV-5 DNA is useful for the synthesis of GURAV, as
 CC diagnostic and probes, for viral gene mapping and for induced plant
 CC disease resistance. It is also useful to detect and quantitate expression
 CC of GURAV in plant tissue prior to use in vegetative propagation, by
 CC detecting the presence of GURAV RNA. (Updated on 06-AUG-2003 to correct
 CC OS field.)
 XX
 SQ Sequence 21 BP; 5 A; 0 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 55.0%; Score 11; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 ACTCCATTCT 19
 Db 18 ACTCCATTCT 8

Search completed: September 14, 2005, 10:19:43
 Job time : 379 secs

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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 09:06:19 / Search time 2413 Seconds
(without alignments)
315.493 Million cell updates/sec

Title: US-10-643-801A-35
Perfect score: 20
Sequence: 1 gcatgcccacatccatctc 20

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 444418

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	70.0	69	AZ456041	AZ456041 IM0258U10
2	65.0	37	AZ514485	AZ514485 IM0361F22
3	65.0	74	BX894771	BX894771 Arabidops
4	60.0	22	AZ828663	AZ828663 2M0105F14
5	60.0	25	AZ658622	AZ658622 1M0535F04
6	60.0	38	TA244G07P	TA244G07P T. brucei
7	60.0	42	AZ818778	AZ818778 2M0089E06
8	60.0	45	AZ402282	AZ402282 1M0169G03
9	60.0	55	AA276119	AA276119 vc36e11.r
10	60.0	55	BP080931	BP080931 BP080931
11	60.0	57	BZ663993	BZ663993 SALK_0276
12	60.0	59	CB173531	CB173531 OR_2028E0
13	60.0	69	AZ594221	AZ594221 1M0406K03
14	60.0	70	AA870012	AA870012 vq10e12.r
15	60.0	70	BG237192	BG237192 sabd04g12.
16	60.0	73	BX991911	BX991911 Forward s
17	60.0	74	BU949033	BU949033 vaa04e11.
18	60.0	76	W57143	W57143 mds4b04.r1
19	60.0	78	AJ714048	AJ714048 AJ714048
20	55.0	19	AZ418201	AZ418201 1M0194M12
21	55.0	19	AZ822954	AZ822954 2M0096M10
22	55.0	19	AZ967656	AZ967656 2M0238M09
23	55.0	27	AZ427595	AZ427595 1M0209G07
24	55.0	28	AZ615744	AZ615744 1M0445B15

C	25	11	55.0	40	8	AZ417928	AZ417928 IM0193L14
	26	11	55.0	47	8	AZ769040	AZ769040 IM0569O13
	27	11	55.0	50	1	AU103440	AU103440 AU103440
	28	11	55.0	50	1	AU103444	AU103444 AU103444
	29	11	55.0	50	1	AU103445	AU103445 AU103445
	30	11	55.0	50	1	AU103448	AU103448 AU103448
	31	11	55.0	54	7	CN868714	CN868714 00116FAO
	32	11	55.0	56	6	CB274124	CB274124 ma189a11.
	33	11	55.0	56	6	AF219060	AF219060 AP219060
	34	11	55.0	60	8	CC156046	CC156046 NFX123 Ba
	35	11	55.0	60	9	CR042871	CR042871 Reverse s
	36	11	55.0	64	6	CB264514	CB264514 54-E02082
	37	11	55.0	65	8	AZ500380	AZ500380 1M0338O08
	38	11	55.0	66	9	CR038728	CR038728 Forward s
	39	11	55.0	68	8	AZ465119	AZ465119 1M0274A22
	40	11	55.0	69	9	CL888998	CL888998 adf93b07.
	41	11	55.0	72	7	CN927075	CN927075 000529AEP
	42	11	55.0	72	8	BH228652	BH228652 106147H0
	43	11	55.0	72	8	CR055514	CR055514 Forward s
	44	11	55.0	73	4	BG866118	BG866118 602789A93
	45	11	55.0	74	8	AZ430790	AZ430790 IM0215K19

ALIGNMENTS

RESULT 1
AZ456041/c 69 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION
1M0258U10 Mouse 10kb plasmid UGCI library Mus musculus genomic
clone UGCI0258U10 R, genomic survey sequence.

ACCESSION
AZ456041
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
1 (bases 1 to 69)
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL

Contact: Robert B. Weis
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0258 row: J column: 10
Seq primer: CACACGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 69.

FEATURES

source
1..69
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCI0258U10"
/sex="male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCI library"
/note="Vector: pMD29mV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 69;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCACTCCCATCTT 20
Db 62 CCACTCCCATCTT 49

RESULT 2
AZ514485 37 bp DNA linear GSS 05-OCT-2000
LOCUS clome UGCGIM0361F2 F, genomic survey sequence.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contract: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: F column: 22
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence step: 37.
Location/Qualifiers
1. 37

FEATURES

Source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0361F22"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

ORIGIN

Query Match 65.0%; Score 13; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTGCCACTCCCAT 16
Db 34 TTGCCACTCCCAT 22

RESULT 3
BX894771 74 bp DNA linear GSS 05-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-683C03-023158.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroside II; Brassicales; Brassicaceae; Arabidopsids.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.
GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
22755829
12874060
2

Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
3

Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 74)
Li, Y., Strizhov, N., Rosso, M.G. and Weishaar, B.
Direct Substitution
Submitted (31-MAR-2004) Weishaar, B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g22840.
Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated

COMMENT

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
Location/Qualifiers

FEATURES
source

1. 74
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-683C03-023158"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 65.0%; Score 13; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATCTT 20
|||
Db 41 CACTCCCATCTT 53

RESULT 4
AZ828663/c 22 bp DNA linear GSS 20-FEB-2001
LOCUS 2M010511R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCG2M0105114 R, genomic survey sequence.

ACCESSION AZ828663
VERSION AZ828663.1 GI:12998571
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: 1 column: 14
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source

1. 22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0105114"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|bp|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 12; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCACTCCCATTC 18
|||
Db 13 CCACTCCCATTC 2

RESULT 5
AZ658622 25 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0535F04R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCG1M0535F04 R, genomic survey sequence.

ACCESSION AZ658622
VERSION AZ658622.1 GI:11795768
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0535 row: 1 column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

FEATURES
source

1. 25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0535F04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 12; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTGCCATTCTT 20
| | | | | | | | | |
| | | | | | | | | |
Db 3 ACTCCCATCTT 14

RESULT 6
LOCUS TA244G07P/c 38 bp DNA linear GSS 13-DEC-2000
DEFINITION T. Brucei sheared genomic DNA clone 244G07, forward sequence,
AL483538
VERSION AL483538.1 GI:11849039
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 38)
AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Mellville, S. E., Rajandream, M. A. and Barrell, B. G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J. C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).

FEATURES

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..38
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRBU927"
/db_xref="taxon:5691"
/clone="244G07"

ORIGIN

Query Match 60.0%; Score 12; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CATTGCCACTCC 13
| | | | | | | | | |
| | | | | | | | | |
Db 21 CATTGCCACTCC 10

RESULT 7
LOCUS AZ818778/c 42 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0089E06F Mouse 10kb plasmid UNGCM library Mus musculus genomic
clone UNGC2M0089E06 F, genomic survey sequence.
ACCESSION AZ818778
VERSION AZ818778.1 GI:1298866
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 42)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
TEL: 801 585 5606
FAX: 801 585 7177
EMAIL: ddunn@genetics.utah.edu
INSERT LENGTH: 10000 Std Error: 0.00
PLATE: 0089 ROW: B COLUMN: 06
SEQ PRIMER: CGTGTAAACGACGCCACGT
CLASS: plasmid ends
HIGH QUALITY SEQUENCE STOP: 42.

FEATURES

Location/Qualifiers
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNGCM0089E06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UNGCM library"
/vector="Vector: pMD20V; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 12; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;

	Matches	12; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	7	CCACTCCCATTC	18						
Db	13	CCACTCCCATTC	2						

RESULT	8
AZ402282/c	
LOCUS	
DEFINITION	
<hr/>	
AZ402282	45 bp DNA linear GSS 03-OCT-2000
IM016SG03R Mouse 10kb plasmid UUC1M library Mus musculus genomic	
clone UUCG1M0169503 R, genomic survey sequence.	

ACCESSION	AZ402282	
VERSION	AZ402282.1	GI:10517356
KEYWORDS	GSS.	
SOURCE	Mus musculus	(house mouse)
ORGANISM	Mus musculus	

REFERENCE
AUTHORS
1 (bases 1 to 45)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
et al. 1994. National Cancer Institute. *Database of Human Gene*

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0169 row: G column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 45.

FEATURES	Location/Qualifiers
source	1. .45
	/occurrence="Mus muscu]us"

`/lab host="". Coli strain XL10-gold, T1-resistant, F-"`
`/clone lib="Mouse 10kb plasmid U98CCL library"`
`/note="Vector: PMD42mv; Purified genomic DNA from M.`
`musculus C57BL/6J (male) was obtained from the Jackson`
`Laboratory Mouse DNA Resource`
`(http://www.jax.org/resources/documents/dnares/). The DNA`
`was hydrodynamically sheared by repeated passage through a`
`0.005 inch orifice at constant velocity. The sheared DNA`
`was blunt end-repaired with T4 DNA polymerase and T4`
`polynucleotide kinase. Adaptor oligonucleotides were`
`ligated to the blunt ends in high molar excess. The`
`adaptor DNA was purified and size-selected for a 9.5 to`
`10.5 kb range using preparative agarose gel`
`electrophoresis. Vector DNA was prepared from a derivative`
`of PMD42 (gi|4732114|gb|AF12907.1), a copy-number`
`inducible derivative of plasmid RL1. The vector was ligated`
`with adaptors complementary to the insert adaptors and`
`purified. The sheared, adaptor mouse DNA was annealed to`
`adaptor vector DNA, and transformed into`
`chemically-competent E. coli XL10-gold (Stratagene) cells`
`and selected for ampicillin resistance."`

Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	7	CCACTCCCAATTC	18						
Db	35	CCACTCCCAATTC	24						

[illegible]

ACCESSION	AA276119	GI:1918749
VERSION	AA276119.1	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE	1 (bases 1 to 55)
AUTHORS	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

JOURNAL COMMENT
Unpublished (1996)
Contact: Marra M/Mouse EST Project
http://www.marra.com

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.jlnl.gov) for further information.
MGI:469540
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2. ET from Amerham
High quality sequence stop: 1.

```

FEATURES
source      Location/Qualifiers
1. .55     /source="http://www.murci.com"

```

```

/tissue_type="Kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"
/clone_id="Barstead MpuRB1"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15'
TGTACGATCGATCGAAGCGAGCGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3'; double-stranded cDNA was ligated to Eco RI adaptors
[CATGATTCGATNCC], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead."

```

ORIGIN

Query Match	60.0%	Score 12;	DB 1;	length 55;
Best Local Similarity	100.0%	Pred. No.	1.5e+04;	
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	8	CACTCCCATTTCT	19
Db	21	CACTCCCATTTCT	32

```

RESULT 10
BP080931/c
LOCUS      BP080931      55 bp      mRNA      linear      EST 27-AUG-2004
DEFINITION BP080931 Lotus japonicus roots Lotus corniculatus var. japonicus
            CDNA clone MR064f09_f_3', mRNA sequence.
ACCESSION  BP080931
VERSION     BP080931.1
KEYWORDS   GI:45637592
SOURCE      EST
ORGANISM   Lotus corniculatus var. japonicus (Lotus japonicus)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
            Lotus.
            1 (bases 1 to 55)
REFERENCE  Asamizu, F., Nakamura, Y., Sato, S. and Tabata, S.
AUTHORS   Characteristics of the Lotus japonicus Gene Repertoire Deduced from
TITLE      Large-Scale Expressed Sequence Tag (EST) Analysis
JOURNAL    Plant Mol. Biol. 54 (3), 405-414 (2004)
COMMENT    Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kasarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
            Location/Qualifiers
                1..55
                /organism="Lotus corniculatus var. japonicus"
                /mol_type="mRNA"
                /isolate="Miyakojima MG-20"
                /db_xref="taxon:34305"
                /clone="MR064f09_f_3"
                /issue_type="Roots"
                /clone_1lb="Lotus japonicus roots"

ORIGIN
Query Match      60.0%; Score 12; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TTGCCACTCCCA 15
Db      43 TTGCCACTCCCA 32

RESULT 11
BZ663993
LOCUS      BZ663993      57 bp      DNA      linear      GSS 31-JUN-2003
DEFINITION BZ663993.43.05.x Arabidopsis thaliana TDNA insertion line
            Arabidopsis thaliana genomic clone SALK_027603.43.05.x, genomic
            survey sequence.
ACCESSION  BZ663993
VERSION     BZ663993.1
KEYWORDS   GI:28180086
SOURCE      GSS
ORGANISM   Arabidopsis thaliana (thale cress)
            Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 57)
REFERENCE  Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
AUTHORS   Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
            Shim, P., Zimmerman, J. and Ecker, J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL    Arabidopsis Genome
COMMENT    Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of

```

```

            TDNA.
            Class: TDNA tagged.
            Location/Qualifiers
                1..57
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /ecotype="Col-0"
                /db_xref="taxon:3702"
                /clone="SALK_027603.43.05.x"
                /note="1lb="Arabidopsis thaliana TDNA insertion lines"
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocol used can
            be found at http://signal.salk.edu/tdna_protocol.html"

ORIGIN
Query Match      60.0%; Score 12; DB 8; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ATTGCCACTCCC 14
Db      18 ATTGCCACTCCC 29

RESULT 12
CB173531/c
LOCUS      CB173531      59 bp      mRNA      linear      EST 09-OCT-2003
DEFINITION CB173531 OR_2028E03 010501.y1 Adult mouse olfactory epithelium library Mus
            musculus CDNA clone 2028E03 5', mRNA sequence.
ACCESSION  CB173531
VERSION     CB173531.1
KEYWORDS   GI:37592160
SOURCE      EST.
ORGANISM   Mus musculus (house mouse)
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 59)
REFERENCE  Young, J.M., Shykind, B.M., Lane, R.P., Tomnes-Priddy, L., Ross, J.A.,
AUTHORS   Walker, M., Williams, E.M. and Trask, B.J.
TITLE      Odorant receptor expressed sequence tags demonstrate olfactory
            expression of over 400 genes, extensive alternate splicing and
            unequal expression levels
JOURNAL    Genome Biol. 4 (11), R71.1-R71.15 (2003)
COMMENT    Contact: Young JM
            Trask Lab, Division of Human Biology
            Fred Hutchinson Cancer Research Center
            1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
            98109-1024 USA
            Tel: 206 667 1471
            Fax: 206 667 6524
            Email: jayoung@fhcrc.org
            Seq primer: M13 Reverse.
            Location/Qualifiers
                1..59
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /clone="2028E03"
                /issue_type="Olfactory and respiratory epithelium"
                /dev_stage="Adult"
                /note="Organ: Olfactory epithelium library"
            LambdaZAPII-XR, Site 1: EcoRI; Site 2: XhoI. This library
            was provided by Leslie Vosehall. mRNA was prepared from
            the olfactory and respiratory epithelium of an adult
            mouse. Oligo-dT primed cDNA was directionally cloned into
            Stratagene's lambdaZAPII-XR vector."

ORIGIN
Query Match      60.0%; Score 12; DB 6; Length 59;

```


RESULT 15
BG237192

LOCUS BG237192 70 bp mRNA linear EST 23-JUL-2004
 DEFINITION bab04q12.y1 Gm-cl071 glycine max cdna clone GENOME SYSTEMS CLONE
 ID: Gm-cl071-719 5', mRNA sequence.

ACCESSION BG237192
 VERSION BG237192.1 GI:12772265
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosoid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine

REFERENCE
AUTHORS

1 (bases 1 to 70)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvett, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, T., Underwood, K., Steppe, M., Theising, B., Allen, M.,
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,
 Schurr, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)

JOURNAL
COMMENT

Contact: Shoemaker R./Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. Putative full
 length read vector to vector length is 71. This clone is available
 through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA
 (phone: 800 423 4163; email: info@biogeneticservices.com).

FEATURES
source

1..70
 Location/Qualifiers

/organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl071-719"
 /issue_type="Immature pods (-2cm long) of greenhouse
 grown plants"
 /lab_host="DH10B"
 /clone_id="Gm-cl071"
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; The
 cDNA library was constructed from mRNA isolated from
 immature pods (approximately 2cm long) of greenhouse grown
 plants. The library was prepared using the Ligo
 Technologies superscript cDNA library construction kit.
 Complementary DNA was synthesized from mRNA using a
 poly(dT) sequence with a NotI restriction site. SalI
 linkers adapters were ligated to the blunt-ended cDNA
 fragments followed by NotI digestion. The cDNA fragments
 were directionally cloned into the NotI-SalI restriction
 site of the pSPORT1 vector. The ligated cDNA fragments
 were transformed into E.coli Electromax DH10B host cells.
 This library was constructed in the laboratory of Dr. Lila
 Vodkin by Ann Khanna at the University of Illinois at
 Urbana-Champaign. email: l-vodkin@uiuc.edu"

ORIGIN

Query Match 60.0%; Score 12; DB 4; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCACCTCCCAT 16
 |||||

DB 19 TGCACCTCCCAT 30

RESULT 16
BX991911/c

LOCUS BX991911/c 73 bp DNA linear GSS 05-JUL-2004
 DEFINITION Forward strand read from insert in 3'HPT insertion targeting and
 chromosome engineering clone MHP384e03, genomic survey sequence.

ACCESSION BX991911
 VERSION BX991911.1 GI:49723369
 KEYWORDS GSS; genome survey sequence; MICEP.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 73)

REFERENCE
AUTHORS

Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
 Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
 Rogers, J. and Bradley, A.
 Direct Submissions
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICEP
 Location/Qualifiers

JOURNAL
COMMENT

1..73
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHP384e03"
 /clone_id="MHP3"

FEATURES
source

1..73
 Location/Qualifiers

/organism="Canis familiaris"
 /mol_type="mRNA"
 /cultivar="Williams"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl071-719"
 /issue_type="Immature pods (-2cm long) of greenhouse
 grown plants"
 /lab_host="DH10B"
 /clone_id="Gm-cl071"
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; The
 cDNA library was constructed from mRNA isolated from
 immature pods (approximately 2cm long) of greenhouse grown
 plants. The library was prepared using the Ligo
 Technologies superscript cDNA library construction kit.
 Complementary DNA was synthesized from mRNA using a
 poly(dT) sequence with a NotI restriction site. SalI
 linkers adapters were ligated to the blunt-ended cDNA
 fragments followed by NotI digestion. The cDNA fragments
 were directionally cloned into the NotI-SalI restriction
 site of the pSPORT1 vector. The ligated cDNA fragments
 were transformed into E.coli Electromax DH10B host cells.
 This library was constructed in the laboratory of Dr. Lila
 Vodkin by Ann Khanna at the University of Illinois at
 Urbana-Champaign. email: l-vodkin@uiuc.edu"

JOURNAL
COMMENT

Contact: Skip Virgin
 RNA Expression in Diseased Tissues by RDA
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

Library was constructed by Tianxiang Shen and Skip Virgin DNA
 sequencing by: Washington University Genome Sequencing Center for
 information on obtaining a clone please contact: Skip Virgin
 (virgin@immunology.wustl.edu)
 Seq primer: -40RP from Gidco.

Location/Qualifiers

1..74
 Location/Qualifiers

FEATURES
source

/organism="Canis familiaris"

/mol_type="mRNA"
/db_xref="taxon:9615"
/tissue_type="Brain from a dog with encephalitis"
/lab_host="DH5a"
/clone_lib="SV DOGRDA RD3"
/note="Vector: PCR2.1-TOPO. PCR products were directly cloned into TA cloning vector (pre-cut vector PCR2.1-TOPO was purchased from Invitrogen) Average insert size is 300bp. Our insert also have same adaptor sequence on both ends. The sequence of the adaptor is:
5'-ATACGTGACGCTGCTTACATCTG-3'."

ORIGIN

Query Match 60.0%; Score 12; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCATCTC 13
Db 17 CATTGCCATCTC 6

RESULT 18 76 bp mRNA linear EST 04-JUN-1996
W57143/c clone IMAGE:372175 5' similar to PIR:S54157 S54157 extensin-like protein - cowpea ;, mRNA sequence.

ACCESSION W57143.1 GI:1359002
VERSION W57143.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus. 1 (bases 1 to 76)

AUTHORS Marra,M., Haller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMNI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watsn.wustl.edu
This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:233607

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: ETPRimer
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

1..76
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:372175"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NBMEL3.5 14.5"
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I, Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', GTTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTT

T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 1; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization, and was constructed by Benito Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 60.0%; Score 12; DB 7; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATCTT 19
Db 76 CACTCCCATCTT 65

RESULT 19 78 bp mRNA linear EST 30-JUN-2004
AJ714048/c clone LKPD01 Homo sapiens cDNA clone LKPD02463, mRNA sequence.
LOCUS AJ714048
DEFINITION AJ714048
ACCESSION AJ714048
VERSION AJ714048.1 GI:49499660
KEYWORDS EST.
SOURCE Homo sapiens (human)
Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 78)

REFERENCE Depicta,C., Tombolan,L., Kronmle,G., Romualdi,C., Vitulo,N., Basso,G. and Lanfranchi,G.
A leukemia-enriched cDNA microarray platform identified new transcripts with relevance to the biology of leukemias

JOURNAL Unpublished (2004)
COMMENT Contact: Depicta C
Biology and CRIBI
University of Padova
Via U. Bassi, 58/B, 35131, ITALY.

FEATURES
source Location/Qualifiers

1..78
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LKPD02463"
/tissue_type="bone marrow"
/clone_lib="LKPD01"
/note="Caucasian"

ORIGIN

Query Match 60.0%; Score 12; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCCACTCCCAT 16
Db 61 TGCCACTCCCAT 50

RESULT 20 19 bp DNA linear GSS 03-OCT-2000
AZ418201/c clone U0GCM0194M12 F, genomic survey sequence.
LOCUS AZ418201
DEFINITION AZ418201
ACCESSION AZ418201.1 GI:10542214
VERSION AZ418201.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus. 1 (bases 1 to 19)

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0194 row: M column: 12
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19

FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0194M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gblAF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 CTCGCATTCTT 20
|||||||
Db 7 CTCGCATTCTT 17
|||||||

RESULT 21
AZ822954/c
LOCUS
DEFINITION
2M009611OR Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0096110 R, genomic survey sequence.
ACCESSION
AZ822954
VERSION
AZ822954.1 GI:12992862
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: I column: 10
Seq primer: CACACAGAAACGCGTAGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19

FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0096110"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gblAF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 CCACTCCATT 17
|||||||
Db 15 CCACTCCATT 5
|||||||

RESULT 22
AZ967656/c
LOCUS
DEFINITION
2M0238M09R Mouse 10kb plasmid UUCG2M library Mus musculus genomic
clone UUCGCM0238M09 R, genomic survey sequence.
ACCESSION
AZ967656
VERSION
AZ967656.1 GI:13838883
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0238 row: M column: 09
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0238M09"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number.
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 55.0%; Score 11; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCAT 17
|||
Db 16 CCACTCCCAT 6

RESULT 23
AZ427595/c 27 bp DNA linear GSS 03-OCT-2000
LOCUS AZ427595 Mouse 10kb plasmid UUC2M library Mus musculus genomic
DEFINITION clone UUC2M0209G07 R, genomic survey sequence.
ACCESSION AZ427595
VERSION AZ427595.1 GI:10551608
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0209 row: G column: 07
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0209G07"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number.
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 55.0%; Score 11; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCAT 17
|||
Db 17 CCACTCCCAT 7

RESULT 24
AZ615744/c 28 bp DNA linear GSS 13-DEC-2000
LOCUS AZ615744 Mouse 10kb plasmid UUC2M library Mus musculus genomic
DEFINITION clone UUC2M0445B15 F, genomic survey sequence.
ACCESSION AZ615744
VERSION AZ615744.1 GI:11737934
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Petersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tinsley, A., von
Niederkhausen, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss

COMMENT

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0445 row: B column: 15
Seq primer: CGTGTAAACGACGCCACAT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1. .28

Source

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/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0445B15"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnars/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gB]/AF129072.1)', a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

ORIGIN

```

Query Match          55.0%; Score 11; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.Se+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCACTGCCATT 17
    |||||
Db 26 CCACTGCCATT 16

```

26 CCACTCCGATT 16

RESULT	LOCUS	DEFINITION	ACCSSION VERSION	KEYWORDS	SOURCE	ORGANISM
25	A2417928/c					
	A2417928	40 bp DNA linear GSS 03-OCT-2000	IM01331L4R Mouse 10kb plasmid UUCCLM library Mus musculus genomic clone UUCGCM0193JL4 R, genomic survey sequence.	A2417928		
				A2417928.1 GI:10541941 GSS.	Mus musculus (house mouse)	Mus musculus

ORGANISM

REFERENCE

1 (bases 1 to 40)

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
Mammalia; Insectera; Chiroptera; Craniata; Vertebrata; Euteleostomi;
Chordata; Mollusca; Lophotrochozoa; Nemertea; Platyhelminthes;

REFERENCE

AUTHORS

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Bacorin, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meinen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhuesner, A. and Wright, D., Weiss, R.
TITLE
Mice whose whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Published (2000)
COMMENT
Contact: Robert B. Weiss

COMMENT

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0193 row: L column: 14
Seq primer: CACACAGGAAACACGCTTCAC
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
1. 40
source

Source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM10193L14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g14732114[gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match	55.0%;	Score 11;	DB 8;	Length 40;
Best Local Similarity	100.0%;	Pred. No. 5.7e+04;		
Matches	11;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	7	CCACTTCCCATTT	17	
Db	24	CCACTTCCCATTT	14	

22

RESULT 26	
A2769040	
LOCUS	
DEFINITION	A2769040 47 bp DNA linear GSS 16-FEB-2001
ACCESSION	U0559013F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
VERSION	clone UGCGIM0569013 F, genomic survey sequence.
KEYWORDS	A2769040.1 GI:12886765
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

ORGANISM

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 47)

REFERENCE

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
Contact: Robert B. Weis
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0569 row: 0 column: 13
Seq primer: CGTTGTAAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers

FEATURES
source
1..47
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UTGCM0569013"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 55.0%; Score 11; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
9 ACTCCCATCT 19
|||||||
21 ACTCCCATCT 31

Db
21 ACTCCCATCT 31

RESULT 27
AUI03440 50 bp mRNA linear EST 28-JAN-2004
AUI03440
LOCUS
DEFINITION
HEP01378, mRNA sequence.
AUI03440
VERSION
AUI03440.1 GI:13552961
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)

AUTHORS
Suzuki, Y., Tajira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
11375929

JOURNAL
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP03841"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 55.0%; Score 11; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
4 TTGCCACTCCC 14
|||||||
26 TTGCCACTCCC 36

Db
26 TTGCCACTCCC 36

RESULT 28
AUI03444 50 bp mRNA linear EST 28-JAN-2004
AUI03444
LOCUS
DEFINITION
HEP03841, mRNA sequence.
AUI03444
VERSION
AUI03444.1 GI:13552965
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
Suzuki, Y., Tajira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
11375929

JOURNAL
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP03841"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 55.0%; Score 11; DB 1; Length 50;
 Best Local Similarity 100.0%; Pred. No. 5.8e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCC 14
 |||||
 31 TTGCCACTCCC 41

Db

RESULT 29
 AU103445 50 bp mRNA linear EST 28-JAN-2004
 LOCUS AU103445
 DEFINITION AU103445 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HEP03842, mRNA sequence.
 ACCESSION AU103445
 VERSION AU103445.1 GI:13552966
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

TITLE Location/Qualifiers
 JOURNAL MEDLINE
 PUBMED 21270072
 COMMENT EMBL Rep. 2 (5), 388-393 (2001)
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 source 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEP03842"

ORIGIN
 Query Match 55.0%; Score 11; DB 1; Length 50;
 Best Local Similarity 100.0%; Pred. No. 5.8e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCC 14
 |||||
 26 TTGCCACTCCC 36

Db

RESULT 30
 AU103448 50 bp mRNA linear EST 28-JAN-2004
 LOCUS AU103448
 DEFINITION AU103448 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HEP05740, mRNA sequence.
 ACCESSION AU103448
 VERSION AU103448.1 GI:13552969
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

TITLE Location/Qualifiers
 JOURNAL MEDLINE
 PUBMED 21270072
 COMMENT EMBL Rep. 2 (5), 388-393 (2001)
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 source 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEP05740"

ORIGIN
 Query Match 55.0%; Score 11; DB 1; Length 50;
 Best Local Similarity 100.0%; Pred. No. 5.8e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCC 14
 |||||
 39 TTGCCACTCCC 49

Db

RESULT 31
 CN868714 54 bp mRNA linear EST 03-JUN-2004
 LOCUS CN868714
 DEFINITION 001116AAOA002279RT (AAOA) Royal Gala phloem Malus x domestica cDNA
 clone AAOA002279, mRNA sequence.
 ACCESSION CN868714
 VERSION CN868714.1 GI:48126250
 KEYWORDS EST.
 SOURCE Malus x domestica (cultivated apple)
 ORGANISM Malus x domestica

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eustosids I; Rosales; Rosaceae; Maloideae; Malus.
 1 (bases 1 to 54)
 Beuning, L., Bowen, J., Crowhurst, R., Glaeve, A., Jansen, B.,
 McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Vauk, Y.
 HortResearch Apple EST Project
 Unpublished (2004)
 Contact: Gleave, A.
 Sequencing Facility
 The Horticulture and Food Research Institute of New Zealand Ltd
 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
 Tel: 00 64 09 815 4200
 Fax: 00 64 09 815 4201
 Email: est@hortresearch.co.nz.

TITLE Location/Qualifiers
 JOURNAL MEDLINE
 PUBMED 21270072
 COMMENT EMBL Rep. 2 (5), 388-393 (2001)
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 source 1..54
 /organism="Malus x domestica"
 /mol_type="mRNA"
 /db_xref="taxon:3750"
 /clone="AAOA002279"
 /tissue_type="Phloem, scrapings from inside of bark mature
 wood"
 /clone_lib="(AAOA) Royal Gala phloem"
 /note="Vector: pBluescript SK(-); Library sequenced by
 Genesis Research & Development"

ORIGIN
 Query Match 55.0%; Score 11; DB 7; Length 54;
 Best Local Similarity 100.0%; Pred. No. 5.8e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TGGCACTCCCA 15
 |||||
 Db 19 TGGCACTCCCA 29

RESULT 32

CB274124 56 bp mRNA linear EST 24-FEB-2003
 CB274124
 IMAGE:6448532 5', mRNA sequence.

DEFINITION CB274124.1 GI:28464447
 CB274124.1
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS McCarey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,
 1 (bases 1 to 56)
 Martin, J., Wylie, T., Danie, M., Bowers, Y., Theising, B., Gibbons, M.,
 Rutter, E., Tsagaris, R., Ronko, I., Maguire, L., Kennedy, S.,
 Bennett, J., Waterston, R. and Wilson, R.

NIHES Mouse
 Unpublished (2002)
 Contact: McCarey/Eddy NIHES Mouse
 NIHES Mouse

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: east@wustl.wustl.edu
 Library constructed and donated by J. McCarey, Ph.D. (Southwest
 Foundation for Biomedical Research, Dept. of Genetics) - excision
 done by E.M. Eddy, Ph.D. (National Institutes of Health, National
 Institute of Environmental Health Sciences).
 MGI:2072492

Seq primer: Primer name ambiguous
 High quality sequence stop: 52.

FEATURES

Source

Location/Qualifiers
 1..56
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:6448532"
 /sex="male"
 /issue_type="round spermatids, pooled from multiple mice"
 /dev_stage="60 day"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="McCarrey Eddy round spermatid"
 /note="Organ: testis; Vector: pBluescript SK+
 (Stratagene); Site_1: XhoII; Site_2: EcoRI; cDNA oligo
 dt-primed [5'-(GA)10-ACTAGTCTCAGTTTCTTTT-3'] and
 directionally cloned using 5' linkers 5'-AATTCGGCGAG-3'
 and 5'-CTCGTCCG-3'. Size selection of >400bp material
 gives average insert size ranging from 1-2 kb. Library was
 mass excised (from lambda-unifAP-XR) and resulting
 single-stranded phagemids were prepiped and transformed
 into DH10B. Library contains 98.5% recombinants.
 References: J. Androl. 20:635-639 and Gene 25:263-269.
 Library constructed and donated by J. McCarey, Ph.D.
 (Southwest Foundation for Biomedical Research, Dept. of
 Genetics); excision done by E.M. Eddy, Ph.D. (National
 Institutes of Health, National Institute of Environmental
 Health Sciences). Original lambda-based library is
 available through ATCC, catalog #63423."

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 56;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACT 11
 |||||
 Db 38 GCATTGCCACT 48

RESULT 33

AF219060/c 56 bp DNA linear GSS 17-APR-2000
 AF219060
 AF219060 Human Homo sapiens genomic clone Gf9, genomic survey
 sequence.

ACCESSION AF219060 GI:7581506
 AF219060.1
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS Hamshere, M., Cross, S., Daniels, M., Lennon, G. and Brook, J.D.
 1 (bases 1 to 56)
 A transcript map of a 10-Mb region of chromosome 19: A source of
 genes for human disorders, including candidates for genes involved
 in asthma, heart defects, and eye disorders
 Genomics 63 (3), 425-429 (2000)

JOURNAL MEDLINE
 PUBMED
 20171383
 10704290

CONTACT: Hamshere M
 Institute of Genetics
 University of Nottingham
 Queen's Medical Center, Nottingham, NG7 2UL, United Kingdom
 Class: exon-trapped.

FEATURES

Source

Location/Qualifiers
 1..56
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Gf9"
 /clone_lib="Human"

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 56;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTCGCATTCTT 20
 |||||
 Db 52 CTCGCATTCTT 42

RESULT 34

CC156046/c 60 bp mRNA linear GSS 01-APR-2004
 CC156046
 NFX123 BayGenomics Gene Trap Library pGTLdelta.Tmpfs Mus musculus
 cDNA, mRNA sequence.

ACCESSION CC156046 GI:46014502
 CC156046.2
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS BayGenomics.
 TITLE http://baygenomics.ucsf.edu/
 JOURNAL Unpublished (2001)

COMMENT On Apr 1, 2004 this sequence version replaced gi:30109402.
 Contact: BayGenomics
 Bay Area Functional Genomics Consortium (BayGenomics)
 Email: info@baygenomics.ucsf.edu
 Sequence tag generated by 5' RACE of total RNA from gene trap ES
 cell line. ES cell lines harboring insertion mutation of target
 gene are available upon request from BayGenomics. Annotation
 information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?
 OPTION=EXACT&TYPE=CELL_LINE&KEY=NPX123
 Class: Gene trap.

FEATURES
 source
 location/Qualifiers
 1..60

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 oia"
 /db_xref="taxon:10090"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /clone_lib="BayGenomics Gene Trap Library
 pGTRdelta.TMpts"
 /note="Vector: pGTRdelta.TMpts"

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 60;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TGGCACTCCCA 15
 Db 22 TGGCACTCCCA 12

RESULT 35
 LOCUS CR042871/c 60 bp DNA linear GSS 05-JUL-2004
 DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and
 ACCESSION CR042871
 VERSION CR042871.1 GI:49775926
 KEYWORDS GSS; genome survey sequence; MICEP.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
 Rogers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
 Jones, J., and Bradley, A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICEP
 FEATURES
 source
 location/Qualifiers
 1..60
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone_lib="MHP272c17"
 /clone_lib="MHP"

ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 60;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TGGCACTCCCA 15
 Db 30 TGGCACTCCCA 20

RESULT 36
 LOCUS CB264514 64 bp mRNA linear EST 06-NOV-2003
 DEFINITION 54-B020827-035-004-P01q-T7R MPZ-MPZ-ADIS-035 Arabidopsis thaliana cDNA
 ACCESSION CB264514
 VERSION CB264514.1 GI:32889287
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 64)
 Schmidt, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
 Mitchell-Olds, T. and Weishaar, B.
 Large-scale identification and analysis of genome-wide
 single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
 Genome Res. 13 (6), 1250-1257 (2003)
 22683290
 PUBMED
 12799357

COMMENT

Contact: Weishaar B
 ADIS DNA core facility at MPZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpz-koeln.mpg.de
 Insert length: 64 Std Error: 0.00
 plate: 4 row: P column: 01
 Seq primer: T7R; CTATACGACTCACTATAGGA.
 Location/Qualifiers
 1..64

FEATURES
 source

/organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /cultivar="Achkarren-2 (Ak-2)"
 /db_xref="GABI:594855"
 /db_xref="taxon:3702"
 /clone="MPZp2000P014Q"
 /tissue_type="inflorescence"
 /lab_host="E. coli TOP10"
 /clone_lib="MPZ-ADIS-035"
 /note="Vector: pSPOR1; Site 1: SalI; Site 2: NotI; cDNA
 library from Arabidopsis thaliana, accession Achkarren-2;
 inflorescences from flower buds to young siliques; library
 was made at the Max-Planck-Institute for Plant Breeding
 Research, Cologne, Germany; cloning sites SalI-NotI,
 T7-SalI-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-SF6; Note:
 Sequencing granted in the context of the GABI Arabidopsis
 Verbund1: Genetic diversity, 'establishment of
 high-efficiency SNP-based mapping tools and development of
 methods for genome-wide mutation detection' PI Bernd
 Weisshar; Sequence database: http://gabi.rzp.de This clone
 is available from RZPD; contact RZPD (clone@rzpd.de) for
 further information."

ORIGIN

Query Match 55.0%; Score 11; DB 6; Length 64;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 CTCCATTCTT 20
 Db 34 CTCCATTCTT 44

RESULT 37
 LOCUS AZ500380/c 65 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0338008R Mouse 10kb plasmid UNGCM library Mus musculus genomic
 ACCESSION AZ500380
 VERSION AZ500380.1 GI:10680138
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 65)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tilney, A., von
 Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL Plasmid inserts
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 038 row: 0 column: 08
 Seq primer: CACACAGAAACACCTATGACC
 Class: plasmid ends
 High quality sequence stop: 65.

FEATURES
 Source

1..65
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0338008"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 65;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACCTCCCAT 17
 |||||
 Db 58 CCACCTCCCAT 48

RESULT 38
 CR038728/c 66 bp DNA linear GSS 05-JUL-2004
 LOCUS Forward strand read from insert in 3'HPRT insertion targeting and
 DEFINITION chromosome engineering clone MHP15n17, genomic survey sequence.
 ACCESSION CR038728
 VERSION GSS; genome survey sequence; M1CER.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 66)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission

JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/M1CER

FEATURES
 Source

1..66
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHP15n17"
 /clone_1lb="MHP1"

ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 66;
 Best Local Similarity 100.0%; Pred. No. 5.9e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCCACTCCCA 15
 |||||
 Db 33 TGCCACTCCCA 23

RESULT 39
 AZ465119/c 68 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0274A22R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 DEFINITION clone UUC1M0274A22 R, genomic survey sequence.
 ACCESSION AZ465119
 VERSION GSS.
 KEYWORDS AZ465119.1 G1:10623244
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 68)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D. Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 UNPUBLISHED (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

REFERENCE

AUTHORS

JOURNAL

COMMENT

Insert Length: 10000 Std Error: 0.00
 Plate: 0274 row: A column: 22
 Seq primer: CACACAGAAACACCTATGACC
 Class: plasmid ends
 High quality sequence stop: 68.

FEATURES
 Source

1..68
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0274A22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 11; DB 8; Length 68;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACCTCCCATTT 17
|||||
Db 67 CCACCTCCCATTT 57

RESULT 40

LOCUS CL888998 69 bp DNA linear GSS 30-AUG-2004
DEFINITION abe93b07.x1 Soybean random, unfiltered genomic library Glycine max
CL888998 genomic survey sequence.
ACCESSION CL888998
VERSION CL888998.1 GI:51632383
KEYWORDS GSS.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 69)
Numberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J., Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and Stacey,G.
Methylation filtered genomic sequences from Glycine max unpublished (2004)
Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
Email: stacey@missouri.edu
LidID: 230
Class: shotgun.

REFERENCE

AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES

SOURCE

1..69
/organism="Glycine max"
/mol_type="genomic DNA"
/cultiyar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="Soybean random, unfiltered genomic library"
/note="Vector: POT2; Site_1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut POT2. LidID: 230"

ORIGIN

Query Match 55.0%; Score 11; DB 9; Length 69;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTCACATTCCTT 20
|||||
Db 48 CTCACATTCCTT 58

RESULT 41

CN927075

LOCUS CN927075 72 bp mRNA linear EST 07-JUN-2004
DEFINITION 000529ABPA002900HT (ABPA) Pinkie expanding leaf Malus x domestica
CN927075 cDNA clone ABPA002800, mRNA sequence.
ACCESSION CN927075
VERSION CN927075.1 GI:48399888
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica

REFERENCE

Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 72)
Beuntyng,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES

Location/Qualifiers

SOURCE

1..72
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="ABPA002800"
/tissue_type="leaf"
/dev_stage="Expanding"
/clone_lib="(ABPA) Pinkie expanding leaf"
/note="Vector: pBR-CMV; Library sequenced by Genesis Research & Development"

ORIGIN

Query Match 55.0%; Score 11; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCC 14
|||||
Db 54 TTGCCACTCCC 64

RESULT 42

LOCUS BH228652 72 bp DNA linear GSS 08-NOV-2001
DEFINITION 1006147H09.2EL.x1 1006 - Rescenu Grid G Zea mays genomic, genomic survey sequence.
ACCESSION BH228652
VERSION BH228652.1 GI:16829902
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 72)
Walbot,V.
Maize genomic sequences found using engineered Rescenu transposon

JOURNAL

Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 723 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006147 row: 8
Class: transposon-tagged.

FEATURES
SOURCE
Location/Qualifiers
1. .72
/organism="Zea mays"
/mol_type="genomic DNA"
/cullivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/issue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI, Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcritpion units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu'; Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 55.0%; Score 11; DB 8; Length 72;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GCCACTCCCAT 16
|||||
6 GCCACTCCCAT 16

Db 6 GCCACTCCCAT 16

RESULT 43
LOCUS CR055514 72 bp DNA linear GSS 05-JUL-2004
DEFINITION Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP136108, genomic survey sequence.
ACCESSION CR055514
VERSION CR055514.1 GI:49788653
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 72)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.
Direct Submision
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA UK. <http://www.sanger.ac.uk/MICR>
Location/Qualifiers
1. .72
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHP136108"
/clone_id="MHP"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTGCCACT 11
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42 GCATTGCCACT 52

Db 42 GCATTGCCACT 52

RESULT 44
LOCUS BG866118 73 bp mRNA linear EST 29-MAY-2001
BG866118

DEFINITION 602784943F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4910987 5', mRNA sequence.
ACCESSION BG866118
VERSION BG866118.1 GI:14216658
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 73)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
<http://image.llnl.gov>
Plate: LLAM10812 row: F column: 12
High quality sequence stop: 73.
Location/Qualifiers
1. .73
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4910987"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NCI_CGAP_SG2"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 55.0%; Score 11; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CATTGCCACTC 12
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42 CATTGCCACTC 52

Db 42 CATTGCCACTC 52

RESULT 45
LOCUS A2430790/c 74 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0215K19F Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0215K19 F, genomic survey sequence.
ACCESSION A2430790
VERSION A2430790.1 GI:10554803
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 74)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 bp

Insert Length: 10000 Std Error: 0.00
 plate: 0315 row: K column: 10

Seq primer: CGTTGTAACAACGACGGCC
Plate: 0215 Row: K Column: 1

Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends

High quality sequen

High quality sequence stop: 74.

FEATURES

Bouice

1.74

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/mol_type="genomic DNA"
/strain="CE7PT/CT"
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/scrain="C5/BL/6J"
/db xref="Taxon:100
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/waxel="CAX01:10090"  
/clone="UUGC1M0215K19"
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sex="Male"
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/lab_host="
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/clone_lib="Mouse 10kb plasmid UUGC1m library"
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/note="Vector: Purified genomic DNA F
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse Resource

(<http://www.tiaa.org/resources/documents/dnares/>) The DNA

ORIGIN

Query Match	Score	DB	Length
55.0%	11	8	74

Best Local Similarity 100.0%; Pred. No. 6e+04;

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 7 CCACTCCCATTT 17

Db 59 CCACTCCCATTT 49

Search completed: September 14, 2005, 11:43:51
Job time : 2421 secs

Job time : 2421 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 09:46:31 / Search time 122 Seconds
(without alignments)
268.242 Million cell updates/sec

Title: US-10-643-801A-35

Perfect score: 20

Sequence: 1 gcatgcccattccattctt 20

Scoring table: OLIGO_NTC
Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1296172

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PTCT.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	65.0	54	US-08-956-171E-2606	Sequence 2606, App
2	13	65.0	54	US-08-781-986A-2606	Sequence 2606, App
3	12	60.0	21	US-09-262-773-113	Sequence 113, App
4	12	60.0	25	US-09-396-196G-64405	Sequence 64405, A
5	12	60.0	25	US-09-396-196G-106332	Sequence 106332, A
6	12	60.0	25	US-09-396-196G-106333	Sequence 106333, A
7	12	60.0	25	US-09-396-196G-106334	Sequence 106334, A
8	12	60.0	29	US-08-846-012A-8	Sequence 8, Appli
9	12	60.0	29	US-09-100-297-8	Sequence 8, Appli
10	12	60.0	39	US-09-052-995-8	Sequence 8, Appli
11	11	55.0	17	US-08-758-306-997	Sequence 997, App
12	11	55.0	18	US-09-690-185A-5	Sequence 5, Appli
13	11	55.0	18	US-08-853-144C-5	Sequence 5, Appli
14	11	55.0	19	US-09-230-186-46	Sequence 46, Appli
15	11	55.0	20	US-09-403-861A-4	Sequence 4, Appli
16	11	55.0	25	US-09-396-196G-26004	Sequence 26004, A
17	11	55.0	25	US-09-396-196G-26005	Sequence 26005, A
18	11	55.0	25	US-09-396-196G-72679	Sequence 72679, A
19	11	55.0	25	US-09-396-196G-91273	Sequence 91273, A
20	11	55.0	25	US-07-834-539A-24	Sequence 24, Appli
21	11	55.0	42	US-08-053-131-32	Sequence 32, Appli
22	11	55.0	42	US-08-645-641-32	Sequence 32, Appli
23	11	55.0	42	US-07-853-408B-32	Sequence 32, Appli
24	11	55.0	42	US-08-096-762-32	Sequence 24, Appli
25	11	55.0	42	US-08-800-353-24	Sequence 24, Appli
26	11	55.0	42	US-08-308-865-32	Sequence 32, Appli
27	11	55.0	42	US-08-308-865-32	Sequence 32, Appli

C 28	11	55.0	42	3	US-09-042-353-200	Sequence 200, App
C 29	11	55.0	42	3	US-08-758-417A-48	Sequence 48, Appl
C 30	11	55.0	42	5	PCT-US92-06185-24	Sequence 24, Appl
C 31	11	55.0	42	5	PCT-US92-10983-32	Sequence 32, Appl
C 32	10	50.0	12	2	US-08-441-887A-59	Sequence 59, Appl
C 33	10	50.0	15	3	US-09-081-666-147	Sequence 147, App
C 34	10	50.0	15	3	US-09-081-646-830	Sequence 830, App
C 35	10	50.0	18	3	US-09-213-719-54	Sequence 54, Appl
C 36	10	50.0	18	4	US-09-422-978-8213	Sequence 8213, Ap
C 37	10	50.0	18	4	US-09-155-885A-267	Sequence 267, App
C 38	10	50.0	19	4	US-09-422-978-5302	Sequence 5302, Ap
C 39	10	50.0	19	4	US-09-696-791-3881	Sequence 3881, Ap
C 40	10	50.0	19	4	US-09-696-791-3882	Sequence 3882, Ap
C 41	10	50.0	20	1	US-10-141-021-15	Sequence 15, Appl
C 42	10	50.0	20	1	US-10-141-103-15	Sequence 15, Appl
C 43	10	50.0	20	1	US-10-141-063-15	Sequence 15, Appl
C 44	10	50.0	20	1	US-10-141-094-15	Sequence 15, Appl
C 45	10	50.0	20	1	US-10-141-060-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-956-171E-2606/C
Sequence 2606, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2606:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2606:
US-08-956-171E-2606

Query Match 65.0%; Score 13; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCAT 16
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DB 47 TTGCCACTCCCAT 35

RESULT 2

US-08-781-986A-2606/c
Sequence 2606, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2606:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-2606

Query Match 65.0%; Score 13; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCAT 16
|||||
DB 47 TTGCCACTCCCAT 35

RESULT 3

US-09-262-773-113
Sequence 113, Application US/09262773
Patent No. 6225451
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ding, Wei
APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
FILE REFERENCE: Myriad 3
CURRENT APPLICATION NUMBER: US/09/262,773

CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 113
LENGTH: 21
TYPE: DNA
ORGANISM: primer
US-09-262-773-113

Query Match 60.0%; Score 12; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
|||||
DB 2 TTGCCACTCCCA 13

RESULT 4

US-09-396-196G-64405
Sequence 64405, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64405
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-64405

Query Match 60.0%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATTGCCACTCC 13
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DB 8 CATTGCCACTCC 19

RESULT 5

US-09-396-196G-106332
Sequence 106332, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 106332
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-106332

Query Match 60.0%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
DB 7 GCATTGCCACTC 18

RESULT 6
US-09-396-196G-106334
; Sequence 106334, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 106333
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-106333

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Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
DB 5 GCATTGCCACTC 16

RESULT 7
US-09-396-196G-106334
; Sequence 106334, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 106334
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-106334

Query Match 60.0%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
DB 3 GCATTGCCACTC 14

RESULT 8
US-08-846-012A-8/c
; Sequence 8, Application US/08846012A
; Patent No. 5807740

GENERAL INFORMATION:
APPLICANT: AMARAL, M. Catherine.
APPLICANT: CHEN, Jin-Long
TITLE OF INVENTION: Regulators of UCP2 Gene Expression
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,012A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-003
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-846-012A-8

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Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
DB 20 TTGCCACTCCCA 9

RESULT 9
US-09-100-297-8/c
; Sequence 8, Application US/09100297
; Patent No. 5849514
; GENERAL INFORMATION:
; APPLICANT: AMARAL, M. Catherine.
; APPLICANT: CHEN, Jin-Long
; TITLE OF INVENTION: Regulators of UCP2 Gene Expression
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,297

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,012
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-100-297-8

Query Match 60.0%; Score 12; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
DB 20 TTGCCACTCCCA 9

RESULT 10
US-09-052-995-8/c
Sequence 8, Application US/09052995
Patent No. 6183956
GENERAL INFORMATION:
APPLICANT: SivaraJa, Mohanram
APPLICANT: Strulovici, Beta
APPLICANT: Flores, Osvaldo A.
TITLE OF INVENTION: High Throughput In Vitro Screening Assay
TITLE OF INVENTION: For Transcription Modulators
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,995
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018781-00060005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-052-995-8

Query Match 60.0%; Score 12; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CACTCCCATCTT 19
DB 27 CACTCCCATCTT 16

RESULT 11
US-08-758-306-997
Sequence 997, Application US/08758306
Patent No. 5807743
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Waizburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 997:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-306-997

Query Match 55.0%; Score 11; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 2.3e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 CATTGCCACTC 12
DB 6 CATUCCACACUC 16

RESULT 12
US-09-690-185A-5/c
Sequence 5, Application US/09690185A
Patent No. 6471964
GENERAL INFORMATION:

APPLICANT: BIERING, EIRIK
 APPLICANT: KROSSOY, BJORN
 TITLE OF INVENTION: DNA ENCODING STRUCTURAL PROTEIN-1 OF INFECTIOUS SALMON
 TITLE OF INVENTION: ANAEMIA VIRUS AND USES THEREOF
 FILE REFERENCE: BIERING
 CURRENT APPLICATION NUMBER: US/09/690,185A
 PRIOR FILING DATE: 2000-10-17
 PRIOR APPLICATION NUMBER: EP99203401.7
 PRIOR FILING DATE: 1999-10-18
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 5
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Infectious salmon anemia virus
 FEATURE:
 NAME/KEY: primer bind
 LOCATION: (1)..(18)
 US-09-690-185A-5

Query Match 55.0%; Score 11; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCCACTCCCA 15
 |||||
 Db 15 TGCCACTCCCA 5

RESULT 13
 US-08-853-164C-5/c
 Sequence 5, Application US/08853164C
 Patent No. 6489163
 GENERAL INFORMATION:
 APPLICANT: Roy, Arun K.
 APPLICANT: Chen, Shuo
 TITLE OF INVENTION: RIBOZYME MEDIATED INACTIVATION OF THE ANDROGEN RECEPTOR
 FILE REFERENCE: 4003.001500
 CURRENT APPLICATION NUMBER: US/08/853,164C
 CURRENT FILING DATE: 1997-05-08
 PRIOR APPLICATION NUMBER: 60/016,590
 PRIOR FILING DATE: 1996-05-08
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 5
 LENGTH: 18
 TYPE: DNA
 ORGANISM: ARTIFICIAL SEQUENCE
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(7)
 OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
 US-08-853-164C-5

Query Match 55.0%; Score 11; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCCACTCCCA 15
 |||||
 Db 13 TGCCACTCCCA 3

RESULT 14
 US-09-230-196-46
 Sequence 46, Application US/09230196
 Patent No. 6307035
 GENERAL INFORMATION:
 APPLICANT: Rauscher III, Frank J.
 APPLICANT: Jensen, David E.
 TITLE OF INVENTION: BRCA1 Associated Protein (BAP-1) and
 TITLE OF INVENTION: Uses Therefor
 NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howson and Howson
 STREET: Spring House Corporate Cntr., PO Box 457
 CITY: Spring House
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19477
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/230,196
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/022,997
 FILING DATE: 02-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/038,109
 FILING DATE: 19-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER: WST688BUSA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9200
 TELEFAX: 215-540-5818
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: other nucleic acid
 US-09-230-196-46

Query Match 55.0%; Score 11; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCAATT 17
 |||||
 Db 6 CCACTCCCAATT 16

RESULT 15
 US-09-403-861A-4/c
 Sequence 4, Application US/09403861A
 Patent No. 6833348
 GENERAL INFORMATION:
 APPLICANT: RICCARDI, Carlo
 TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
 DEATH PATHWAYS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
 STREET: 624 Ninth Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/403,861A
 FILING DATE: 11-Feb-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP98/02490

```

; FILING DATE: 27-APR-1998
; APPLICATION NUMBER: EP 97107033.9
; FILING DATE: 28-APR-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: YUN, Allen C.
;   REGISTRATION NUMBER: 37,971
;   REFERENCE/DOCKET NUMBER: RICCARDI=1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-628-5197
;   TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 20 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1..20
;   OTHER INFORMATION: /note= "PCR reverse primer"
;
; US-09-403-861A-4
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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```

Query Match      55.0%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 TGCCACTGCCA 15
Db      18 TGCCACTGCCA 8

```

```

RESULT 16
US-09-396-196G-26004
; Sequence 26004, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Miltmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   PRIOR FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 26004
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
;
US-09-396-196G-26004

```

```

Query Match      55.0%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GCATTGCCACT 11
Db      15 GCATTGCCACT 25

```

```

RESULT 17
US-09-396-196G-26005
; Sequence 26005, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Miltmann
;   APPLICANT: David Mack

```

```

; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   PRIOR FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 26005
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
;
US-09-396-196G-26005

```

```

Query Match      55.0%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GCATTGCCACT 11
Db      9 GCATTGCCACT 19

```

```

RESULT 18
US-09-396-196G-72679
; Sequence 72679, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Miltmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   PRIOR FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 72679
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
;
US-09-396-196G-72679

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```

Query Match      55.0%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GCATTGCCACT 11
Db      13 GCATTGCCACT 23

```

```

RESULT 19
US-09-396-196G-72680
; Sequence 72680, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Miltmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   PRIOR FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806

```

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 72680
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-72680

Query Match
 Best Local Similarity 55.0%; Score 11; DB 4; Length 25;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCCACT 11
 DB 1 GCATGCCACT 11

RESULT 20
 US-09-396-196G-91273
 Sequence 91273, Application US/09396196G
 Patent No. 6821724
 GENERAL INFORMATION:
 APPLICANT: Michael Miltmann
 APPLICANT: David Mack
 APPLICANT: David Lookhart
 APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 60/100,678
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 91273
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-91273

Query Match
 Best Local Similarity 55.0%; Score 11; DB 4; Length 25;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCCACT 11
 DB 5 GCATGCCACT 15

RESULT 21
 US-07-834-539A-24/C
 Sequence 24, Application US/07834539A
 GENERAL INFORMATION:
 APPLICANT: Lomborg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: William M. Smith
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/834,539A
 FILING DATE: 1992-02-05
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,1223
 REFERENCE/DOCKET NUMBER: 14643-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-543-9600
 TELEFAX: 415-543-5043
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-07-834-539A-24

Query Match
 Best Local Similarity 55.0%; Score 11; DB 1; Length 42;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATTC 18
 DB 11 CACTCCCATTC 1

RESULT 22
 US-08-053-131-32/C
 Sequence 32, Application US/08053131
 Patent No. 5661016
 GENERAL INFORMATION:
 APPLICANT: Lomborg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 197
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 200
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/053,131
 FILING DATE: 26-APR-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,860
 FILING DATE: 16-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/853,408
 FILING DATE: 18-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,1223
 REFERENCE/DOCKET NUMBER: 14643-9-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: DNA (primer)
US-08-053-131-32

Query Match 55.0%; Score 11; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATTC 18
DB 11 CACTCCCATTC 1

RESULT 23

US-08-645-641-32/C
Sequence 32, Application US/08645641
Patent No. 5719032

GENERAL INFORMATION:

APPLICANT: Lomborg, Nils
ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco

STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/645,641
FILING DATE: 20-MAY-1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 14643-000913
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (primer)
US-08-645-641-32

Query Match 55.0%; Score 11; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATTC 18
DB 11 CACTCCCATTC 1

RESULT 24

US-07-853-408B-32/C

Sequence 32, Application US/07853408B
Patent No. 5789650

GENERAL INFORMATION:

APPLICANT: Lomborg, Nils
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 14643-000913
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco

STATE: California
COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 14643-9
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs
TYPE: NUCLEIC ACID

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (primer)
US-07-853-408B-32

Query Match 55.0%; Score 11; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATTC 18
DB 11 CACTCCCATTC 1

RESULT 25

US-08-096-762-32/C
Sequence 32, Application US/08096762
Patent No. 5814318

GENERAL INFORMATION:

APPLICANT: Lomborg, Nils
ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco

STATE: California
COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
US-08-096-762-32

Query Match 55.0%; Score 11; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

Qy 8 CACTCCCATTC 18
Db 11 CACTCCCATTC 1

RESULT 26
US-08-800-353-24/c
Sequence 24, Application US/0800353
Patent No. 5874299
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5874299-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,353
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/834,539
FILING DATE: 1992-02-05
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-800-353-24

Query Match 55.0%; Score 11; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

Qy 8 CACTCCCATTC 18
Db 11 CACTCCCATTC 1

RESULT 27
US-08-308-865-32/c
Sequence 32, Application US/0830865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
US-08-308-865-32

Query Match 55.0%; Score 11; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

Qy 8 CACTCCCATTC 18
Db 11 CACTCCCATTC 1

RESULT 28
US-09-042-353-200/c
Sequence 200, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-200

Query Match 55.0%; Score 11; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 8 CACTCCCATTC 18
DB 11 CACTCCCATTC 1

RESULT 29
US-08-758-417A-48/c
Sequence 48, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-758-417A-48

Query Match 55.0%; Score 11; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 2,4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATTC 18
11 CACTCCCATTC 1

RESULT 30

PCT-US92-06185-24/c
Sequence 24, Application PC/TUS9206185
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06185
FILING DATE: 19910828
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 87654
REFERENCE/DOCKET NUMBER: 14643-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US92-06185-24

Query Match 55.0%; Score 11; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 2,4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATTC 18

Db 11 CACTCCCATTC 1

RESULT 31
PCT-US92-10983-32/c
Sequence 32, Application PC/TUS9210983
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10983
FILING DATE: 19921217
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
PCT-US92-10983-32

Query Match 55.0%; Score 11; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 2,4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATTC 18
11 CACTCCCATTC 1

RESULT 32
US-08-441-887A-59/c
Sequence 59, Application US/08441887A
Patent No. 5837832
GENERAL INFORMATION:
APPLICANT: Chee, Mark
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Hubbard, Earl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

Query Match 55.0%; Score 11; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 2,4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; STREET: Two Embarcadero Center, 8th Floor
; City: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
; US-08-441-887A-59

Query Match
Best Local Similarity 50.0%; Score 10; DB 2; Length 12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCATCCCAT 16
Db 12 CCATCCCAT 3

RESULT 33
US-09-081-646-147/c
; Sequence 147, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 147
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-081-646-147

Query Match
Best Local Similarity 50.0%; Score 10; DB 3; Length 15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; ORGANISM: Homo sapiens
; US-09-081-646-147

Query Match
Best Local Similarity 50.0%; Score 10; DB 3; Length 15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 7 CCATCCCAT 16
Db 11 CCATCCCAT 2

RESULT 34
US-09-081-646-830/c
; Sequence 830, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 830
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-081-646-830

Query Match
Best Local Similarity 50.0%; Score 10; DB 3; Length 15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCATCCCAT 16
Db 11 CCATCCCAT 2
```

```

US-09-213-719-54
; Sequence 54, Application US/09213719B
; Patent No. 6150163
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD44 EXPRESSION
; FILE REFERENCE: RTS-0006
; CURRENT APPLICATION NUMBER: US/09/213,719B
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-213-719-54

Query Match
Best Local Similarity 50.0%; Score 10; DB 3; Length 18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATTGCCACT 11
Db 8 CATTGCCACT 17

RESULT 36
US-09-422-978-8213/c
; Sequence 8213, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
```

```

; ORGANISM: Homo sapiens
; US-09-422-978-8213/c

Query Match
Best Local Similarity 50.0%; Score 10; DB 3; Length 18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.0200C01
; CURRENT APPLICATION NUMBER: US/09/422.978
; EARLIER FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8213
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-14446 for SEQ 348, in compleme
US-09-422-978-8213

Query Match          50.0%; Score 10; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATGCCAC 10
Db      10 GCATGCCAC 1

RESULT 37
US-09-155-885A-267/C
; Sequence 267, Application US/09155885A
; Patent No. 6709812
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 9687053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
;
```

```

; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 267:
US-09-155-885A-267

Query Match          50.0%; Score 10; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CCATCCCAT 16
Db      11 CCATCCCAT 2

RESULT 38
US-09-422-978-5302
; Sequence 5302, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.0200C01
; CURRENT APPLICATION NUMBER: US/09/422.978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5302
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-23334 for SEQ 1368,
US-09-422-978-5302

Query Match          50.0%; Score 10; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCCCATCTT 20
Db      4 TCCCATCTT 13

RESULT 39
US-09-696-791-3881
; Sequence 3881, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3881
; LENGTH: 19
;
```

```
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3881
```

```
Query Match          50.0%; Score 10; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 4 TTGCCACTCC 13
    |||||
Db 9 TTGCCACTCC 18
```

```
RESULT 40
US-09-696-791-3882
/ Sequence 3882, Application US/09696791
/ Patent No. 6770633
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Robbins, Joan M.
```

```
/ TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
```

```
/ FILE REFERENCE: 480124.407
```

```
/ CURRENT APPLICATION NUMBER: US/09/696,791
```

```
/ NUMBER OF SEQ ID NOS: 4523
```

```
/ SOFTWARE: PatentIn Ver. 2.0
```

```
/ SEQ ID NO 3882
```

```
/ LENGTH: 19
```

```
/ TYPE: DNA
```

```
/ ORGANISM: Homo sapiens
```

```
/ FEATURE:
```

```
/ OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3882
```

```
Query Match          50.0%; Score 10; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 4 TTGCCACTCC 13
    |||||
Db 2 TTGCCACTCC 11
```

```
RESULT 41
```

```
US-10-141-021-15/c
```

```
/ Sequence 15, Application US/10141021
```

```
/ Patent No. PPI4777
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: BEINEKE, WALTER F.
```

```
/ TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 4"
```

```
/ FILE REFERENCE: 30034-93461
```

```
/ CURRENT APPLICATION NUMBER: US/10/141,021
```

```
/ NUMBER OF SEQ ID NOS: 18
```

```
/ SOFTWARE: PatentIn Ver. 2.1
```

```
/ SEQ ID NO 15
```

```
/ LENGTH: 20
```

```
/ TYPE: DNA
```

```
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
```

```
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-021-15
```

```
Query Match          50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 ATTGCCACTC 12
    |||||
Db 11 ATTGCCACTC 2
```

```
RESULT 42
US-10-141-103-15/c
/ Sequence 15, Application US/10141103
```

```
/ Patent No. PPI4829
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: BEINEKE, WALTER F.
```

```
/ TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 5"
```

```
/ FILE REFERENCE: 30034-93462
```

```
/ CURRENT APPLICATION NUMBER: US/10/141,103
```

```
/ NUMBER OF SEQ ID NOS: 18
```

```
/ SOFTWARE: PatentIn Ver. 2.1
```

```
/ SEQ ID NO 15
```

```
/ LENGTH: 20
```

```
/ TYPE: DNA
```

```
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
```

```
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-103-15
```

```
Query Match          50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 ATTGCCACTC 12
    |||||
Db 11 ATTGCCACTC 2
```

```
RESULT 43
```

```
US-10-141-063-15/c
```

```
/ Sequence 15, Application US/10141063
```

```
/ Patent No. PPI4839
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: BEINEKE, WALTER F.
```

```
/ TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 10"
```

```
/ FILE REFERENCE: 30034-93467
```

```
/ CURRENT APPLICATION NUMBER: US/10/141,063
```

```
/ NUMBER OF SEQ ID NOS: 18
```

```
/ SOFTWARE: PatentIn Ver. 2.1
```

```
/ SEQ ID NO 15
```

```
/ LENGTH: 20
```

```
/ TYPE: DNA
```

```
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
```

```
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-063-15
```

```
Query Match          50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 ATTGCCACTC 12
    |||||
Db 11 ATTGCCACTC 2
```

```
RESULT 44
```

```
US-10-141-094-15/c
```

```
/ Sequence 15, Application US/10141094
```

```
/ Patent No. PPI4978
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: BEINEKE, WALTER F.
```

```
/ TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 6"
```

```
/ FILE REFERENCE: 30034-93463
```

```
/ CURRENT APPLICATION NUMBER: US/10/141,094
```

```
/ NUMBER OF SEQ ID NOS: 18
```

```
/ SOFTWARE: PatentIn Ver. 2.1
```

```
/ SEQ ID NO 15
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```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-094-15

```

```

Query Match          50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 ATTGCCACTC 12
        |||||
        |||||
Db      11 ATTGCCACTC 2

```

```

RESULT 45
US-10-141-060-15/c
; Sequence 15, Application US/10141060
; Patent No. PP15079
; GENERAL INFORMATION:
; APPLICANT: BEINEKE, WALTER F.
; TITLE OF INVENTION: BLACK WALNUT TREE NAMED "BEINEKE 1"
; FILE REFERENCE: 30034-92642
; CURRENT APPLICATION NUMBER: US/10/141,060
; CURRENT FILING DATE: 2002-07-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-141-060-15

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Query Match          50.0%; Score 10; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 ATTGCCACTC 12
        |||||
        |||||
Db      11 ATTGCCACTC 2

```

Search completed: September 14, 2005, 11:45:54
 Job time : 124 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 10:15:01 ; Search time 482 Seconds
(without alignments)
272.500 Million cell updates/sec

Title: US-10-643-801A-35

Perfect score: 20

Sequence: 1 gcattgccacccattctt 20

Scoring table: OLIGO_NUC

Searched: 7351250 seqs, 3283620254 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8541662

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Listing first 45 summaries

Database:

Published Applications NA:*

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
3: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
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22: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
23: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
24: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
25: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
26: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20 21 US-10-643-801-35	Sequence 35, App1
2	20	100.0	20 21 US-10-643-801-157	Sequence 157, App1
3	15	75.0	20 21 US-10-643-801-36	Sequence 36, App1
4	15	75.0	20 21 US-10-643-801-158	Sequence 158, App1
5	15	75.0	25 21 US-10-719-900-415646	Sequence 415646,
6	13	65.0	25 21 US-10-719-900-136702	Sequence 136702,
7	13	65.0	25 21 US-10-719-900-840616	Sequence 840616,

C	8	13	65.0	25	22	US-10-843-527-86272	Sequence 86272, A
	9	13	65.0	25	22	US-10-843-527-151905	Sequence 151905,
	10	13	65.0	25	22	US-10-719-956-650147	Sequence 650147,
C	11	13	65.0	54	8	US-08-781-986A-2606	Sequence 2606, Ap
C	12	13	65.0	54	18	US-10-329-624-2606	Sequence 2606, Ap
	13	13	65.0	60	10	US-09-908-975-18015	Sequence 18015, A
	14	12	60.0	12	20	US-10-257-017B-267933	Sequence 267933,
	15	12	60.0	12	20	US-10-257-017B-269218	Sequence 269218,
C	16	12	60.0	12	20	US-10-303-635-73	Sequence 73, App1
	17	12	60.0	20	19	US-10-303-635-74	Sequence 74, App1
C	18	12	60.0	20	19	US-10-303-635-192	Sequence 192, App
C	19	12	60.0	20	22	US-10-257-158A-5395	Sequence 5395, Ap
C	20	12	60.0	24	22	US-10-257-158A-762	Sequence 762, App
C	21	12	60.0	25	21	US-10-719-900-198562	Sequence 198562,
	22	12	60.0	25	21	US-10-719-900-264711	Sequence 264711,
	23	12	60.0	25	21	US-10-719-900-305113	Sequence 305113,
	24	12	60.0	25	21	US-10-719-900-903551	Sequence 903551,
C	25	12	60.0	25	21	US-10-719-900-964504	Sequence 964504,
	26	12	60.0	25	21	US-10-719-900-974937	Sequence 974937,
	27	12	60.0	25	21	US-10-809-189-64405	Sequence 64405, A
	28	12	60.0	25	21	US-10-809-189-106332	Sequence 106332,
C	29	12	60.0	25	21	US-10-809-189-106333	Sequence 106333,
C	30	12	60.0	25	21	US-10-809-189-106334	Sequence 106334,
C	31	12	60.0	25	22	US-10-843-527-19523	Sequence 19523, A
	32	12	60.0	25	22	US-10-843-527-20511	Sequence 20511, A
C	33	12	60.0	25	22	US-10-843-527-216202	Sequence 216202,
C	34	12	60.0	25	22	US-10-843-527-217190	Sequence 217190,
C	35	12	60.0	25	22	US-10-719-956-143538	Sequence 143538,
C	36	12	60.0	25	22	US-10-719-956-166560	Sequence 166560,
	37	12	60.0	25	22	US-10-719-956-329530	Sequence 329530,
	38	12	60.0	25	22	US-10-719-956-329531	Sequence 329531,
	39	12	60.0	25	22	US-10-719-956-693459	Sequence 693459,
	40	12	60.0	26	16	US-10-025-806-257	Sequence 257, App
C	41	12	60.0	51	20	US-10-813-638-478	Sequence 478, App
C	42	12	60.0	60	10	US-09-908-975-15069	Sequence 15069, A
C	43	12	60.0	60	10	US-09-908-975-117268	Sequence 117268, A
C	44	11	55.0	13	20	US-10-257-017B-14061	Sequence 14061, A
	45	11	55.0	13	20	US-10-257-017B-14062	Sequence 14062, A

ALIGNMENTS

RESULT 1
US-10-643-801-35
; Sequence 35, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhano
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US
; CURRENT APPLICATION NUMBER: US/10/643, 801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-801-35

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GCATTGCCATCCATTCTT 20
DB 1 GCATTGCCATCCATTCTT 20

RESULT 2

```
US-10-643-801-157/c
; Sequence 157, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-067805
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 157
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-643-801-157
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GCATTGCCACTCCCATTTCTT 20
Db 20 GCATTGCCACTCCCATTTCTT 1
```

```
RESULT 3
US-10-643-801-36
; Sequence 36, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-067805
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-801-36
```

```
Query Match
Best Local Similarity 75.0%; Score 15; DB 21; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GCATTGCCACTCCCA 15
Db 6 GCATTGCCACTCCCA 20
```

```
RESULT 4
US-10-643-801-158/c
; Sequence 158, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-067805
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 158
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
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```
US-10-643-801-158
```

```
Query Match
Best Local Similarity 75.0%; Score 15; DB 21; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GCATTGCCACTCCCA 15
Db 15 GCATTGCCACTCCCA 1
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```
RESULT 5
US-10-719-900-415646
; Sequence 415646, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 415646
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-415646
```

```
Query Match
Best Local Similarity 75.0%; Score 15; DB 21; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 CATTGCCACTCCCAT 16
Db 4 CATTGCCACTCCCAT 18
```

```
RESULT 6
US-10-719-900-136702/c
; Sequence 136702, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 136702
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-136702
```

```
Query Match
Best Local Similarity 65.0%; Score 13; DB 21; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 5 TGCCACTCCCAT 17
Db 23 TGCCACTCCCAT 11
```

```
RESULT 7
US-10-719-900-840616
; Sequence 840616, Application US/10719900
; Publication No. US20050026164A1
```



```

; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 840616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-840616

Query Match          65.0%; Score 13; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCATTGCCACTCC 13
        |||
Db      6 GCATTGCCACTCC 18

RESULT 8
US-10-843-527-86272/c
; Sequence 86272, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 86272
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-86272

Query Match          65.0%; Score 13; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CACTCCCATCTT 20
        |||
Db      18 CACTCCCATCTT 6

RESULT 9
US-10-843-527-151905
; Sequence 151905, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 151905
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: SARS Virus
US-10-843-527-151905

Query Match          65.0%; Score 13; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CACTCCCATCTT 20
        |||
Db      8 CACTCCCATCTT 20

RESULT 10
US-10-719-956-650147
; Sequence 650147, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 659466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 650147
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-650147

Query Match          65.0%; Score 13; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TGCCACTCCCAT 17
        |||
Db      10 TGCCACTCCCAT 22

RESULT 11
US-08-781-986A-2606/c
; Sequence 2606, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 2606:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 54 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-781-986A-2606

Query Match 65.0%; Score 13; DB 8; Length 54;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCAT 16
 DB 47 TTGCCACTCCCAT 35

RESULT 12

US-10-329-624-2606/c
 Sequence 2606, Application US/10329624
 Publication No. US2004003037A1
 GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5256
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1324

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 2606:

SEQUENCE CHARACTERISTICS:

LENGTH: 54 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2606:

US-10-329-624-2606

Query Match 65.0%; Score 13; DB 18; Length 54;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCAT 16
 DB 47 TTGCCACTCCCAT 35

RESULT 13

US-09-908-975-18015
 Sequence 18015, Application US/09908975
 Publication No. US20030165843A1
 GENERAL INFORMATION:

APPLICANT: SHOSHAN, Avi

APPLICANT: WASSERMAN, Alon

APPLICANT: MINTZ, Eli

APPLICANT: FAIGLER, Simcha

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC-

FILE REFERENCE: 36688-0005

CURRENT APPLICATION NUMBER: US/09/908,975

PRIOR FILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: US 60/287,724

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/221,607

NUMBER OF SEQ ID NOS: 32337

SOFTWARE: PatentIn version 3.0

SEQ ID NO 18015

LENGTH: 60

TYPE: DNA

ORGANISM: Homo sapiens

US-09-908-975-18015

Query Match 65.0%; Score 13; DB 10; Length 60;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCAT 16
 DB 4 TTGCCACTCCCAT 16

RESULT 14

US-10-257-017B-267933

Sequence 267933, Application US/10257017B

Publication No. US20040241651A1

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Plepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 267933

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC00000710

US-10-257-017B-267933

Query Match 60.0%; Score 12; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCACTCCCATTC 18
 DB 1 CCACTCCCATTC 12

RESULT 15
US-10-257-017B-269218/C
; Sequence 269218, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Beclin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 269218
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC00001665
US-10-257-017B-269218

Query Match 60.0%; Score 12; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTGCCATCTCT 19
| | | | | | | | | | | | | | | | | | | | | |
Db 12 CACTGCCATCTCT 1

RESULT 16
US-10-303-635-73
; Sequence 73, Application US/10303635
; Publication No. US20040102621A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
; FILE REFERENCE: RTS-0418
; CURRENT APPLICATION NUMBER: US/10/303,635
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 257
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-635-73

Query Match 60.0%; Score 12; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
| | | | | | | | | | | | | | | | | | | | | |
Db 6 GCATTGCCACTC 17

RESULT 17
US-10-303-635-74
; Sequence 74, Application US/10303635
; Publication No. US20040102621A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
; FILE REFERENCE: RTS-0418
; CURRENT APPLICATION NUMBER: US/10/303,635
; CURRENT FILING DATE: 2002-11-21

; NUMBER OF SEQ ID NOS: 257
; SEQ ID NO 74
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-635-74

Query Match 60.0%; Score 12; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
| | | | | | | | | | | | | | | | | | | | | |
Db 9 GCATTGCCACTC 20

RESULT 18
US-10-303-635-192/C
; Sequence 192, Application US/10303635
; Publication No. US20040102621A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
; FILE REFERENCE: RTS-0418
; CURRENT APPLICATION NUMBER: US/10/303,635
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 257
; SEQ ID NO 192
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical Probe Sequence
US-10-303-635-192

Query Match 60.0%; Score 12; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGCCACTC 12
| | | | | | | | | | | | | | | | | | | | | |
Db 15 GCATTGCCACTC 4

RESULT 19
US-10-257-158A-5395/C
; Sequence 5395, Application US/10257158A
; Publication No. US20050142543A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Zlaty, Monib
; APPLICANT: Gerry, Norman P.
; APPLICANT: Favis, Reyna
; APPLICANT: Kiman, Richard
; TITLE OF INVENTION: METHOD OF DESIGNING ADDRESSABLE ARRAY FOR DETECTION OF NUCLEIC A
; FILE REFERENCE: 19603/2834
; CURRENT APPLICATION NUMBER: US/10/257,158A
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/US01/10958
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/197,271
; NUMBER OF SEQ ID NOS: 9544
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5395
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical Probe Sequence
US-10-257-158A-5395

Query Match 60.0%; Score 12; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTC 12
Db 15 GCATTGCCACTC 4

RESULT 20

US-10-257-158A-762/c
; Sequence 762, Application US/10257158A
; Publication No. US20050142543A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Zilvi, Monib
; APPLICANT: Gerry, Norman P.
; APPLICANT: Favis, Reyna
; APPLICANT: Kilman, Richard
; TITLE OF INVENTION: METHOD OF DESIGNING ADDRESSABLE ARRAY FOR DETECTION OF NUCLEIC AC
; FILE REFERENCE: 19603/2834
; CURRENT APPLICATION NUMBER: US/10/257,158A
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/US01/10958
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/197,271
; NUMBER OF SEQ ID NOS: 9544
; SOFTWARE: Patent version 3.1
; SEQ ID NO 762
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical Probe Sequence
US-10-257-158A-762

Query Match

Best Local Similarity 60.0%; Score 12; DB 22; Length 24;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTC 12
Db 19 GCATTGCCACTC 8

RESULT 21

US-10-719-900-198562/c
; Sequence 198562, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 198562
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-198562

Query Match

Best Local Similarity 60.0%; Score 12; DB 21; Length 25;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATTGCCACTCCC 14

Db 13 ATTGCCACTCCC 2

RESULT 22

US-10-719-900-264711
; Sequence 264711, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 264711
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-264711

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GCCACTCCCACTT 17
Db 4 GCCACTCCCACTT 15

RESULT 23

US-10-719-900-305113
; Sequence 305113, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 305113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-305113

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ACTGCCACTCTT 20
Db 11 ACTGCCACTCTT 22

RESULT 24

US-10-719-900-903551
; Sequence 903551, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 903551
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-903551

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACTCCCATCT 19
Db 12 CACTCCCATCT 23

RESULT 25
US-10-719-900-964504/c
Sequence 964504, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
PRIOR FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 964504
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-964504

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCATCTC 12
Db 21 GCATTGCCATCTC 10

RESULT 26
US-10-719-900-974937
Sequence 974937, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
PRIOR FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 974937
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-974937

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCATCTC 12
Db 12 GCATTGCCATCTC 12

Db 5 GCATTGCCATCTC 16

RESULT 27
US-10-809-189-64405
Sequence 64405, Application US/10809189
Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
PRIOR FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64405
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-809-189-64405

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATTGCCATCTCC 13
Db 8 CATTGCCATCTCC 19

RESULT 28
US-10-809-189-106332
Sequence 106332, Application US/10809189
Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
PRIOR FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 106332
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-809-189-106332

Query Match 60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCATCTC 12
Db 7 GCATTGCCATCTC 18

RESULT 29
US-10-809-189-106333

```

; Sequence 106333, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106333
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-106333

```

```

Query Match      60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GCATTGCCACTC 12
Db      5 GCATTGCCACTC 16

```

```

RESULT 30
US-10-809-189-106334
; Sequence 106334, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106334
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-106334

```

```

Query Match      60.0%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GCATTGCCACTC 12
Db      3 GCATTGCCACTC 14

```

```

RESULT 31
US-10-843-527-19523
; Sequence 19523, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
US-10-843-527-19523

```

```

; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 19523
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-19523

```

```

Query Match      60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 CACTCCCATTCCT 19
Db      13 CACTCCCATTCCT 24

```

```

RESULT 32
US-10-843-527-20511
; Sequence 20511, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 20511
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-20511

```

```

Query Match      60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      9 ACTCCCATTCCT 20
Db      2 ACTCCCATTCCT 13

```

```

RESULT 33
US-10-843-527-216202/c
; Sequence 216202, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 216202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-216202

```

```
Query Match          60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTCCCATCTCT 20
   |||||
   |||||
Db 24 ACTCCCATCTCT 13

RESULT 34
US-10-843-527-217190/c
; Sequence 217190, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; FILE REFERENCE: 3602.1
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; CURRENT APPLICATION NUMBER: US/10/843,527
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 217190
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-217190

Query Match          60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACTCCCATCTCT 19
   |||||
   |||||
Db 13 CACTCCCATCTCT 2

RESULT 35
US-10-719-956-143538/c
; Sequence 143538, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; FILE REFERENCE: 3527.1
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 143538
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-143538

Query Match          60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCCACTCCCAT 16
   |||||
   |||||
Db 22 TGCCACTCCCAT 11

RESULT 36
US-10-719-956-166560/c
; Sequence 166560, Application US/10719956
; Publication No. US20040146910A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; FILE REFERENCE: 3527.1
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 166560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-166560

Query Match          60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGCCACTCCCAT 16
   |||||
   |||||
Db 17 TGCCACTCCCAT 6

RESULT 37
US-10-719-956-329530
; Sequence 329530, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; FILE REFERENCE: 3527.1
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 329530
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-329530

Query Match          60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTCCCATCTCT 20
   |||||
   |||||
Db 14 ACTCCCATCTCT 25

RESULT 38
US-10-719-956-329531
; Sequence 329531, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; FILE REFERENCE: 3527.1
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 329531
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-329531
```

Query Match 60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACTCCATCTCT 20
DB 14 ACTCCATCTCT 25

RESULT 39
US-10-719-956-693459
Sequence 693459, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 693459
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-693459

Query Match 60.0%; Score 12; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
DB 2 TTGCCACTCCCA 13

RESULT 40
US-10-025-806-257
Sequence 257, Application US/10025806
Publication No. US20030198955A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Ballinger, Robert
APPLICANT: Kekuda, Rameesh
APPLICANT: Coleman, Steven
APPLICANT: Spytek, Kimberly
APPLICANT: Caaman, Stacie
APPLICANT: Edinger, Shlomit
APPLICANT: Gerlach, Valerie
APPLICANT: Sciore, Paul
APPLICANT: Smithson, Glennada
APPLICANT: Peyman, John
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Vernet, Corine
APPLICANT: Shenoy, Suresh
APPLICANT: Gunther, Erik
APPLICANT: Miller, Isabelle
APPLICANT: Tchernev, Velizar
APPLICANT: Anderson, David
APPLICANT: Gusev, Vladimir
APPLICANT: Malyankar, Uriel
APPLICANT: Zhong, Haihong
APPLICANT: Ellerman, Karen
APPLICANT: Wolenc, Adam
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-224 AB
CURRENT APPLICATION NUMBER: US/10/025,806
CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/256,635
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/259,743
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/299,327
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 60/261,498
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/263,689
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/276,464
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/271,021
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/275,946
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/278,150
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/285,718
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 60/312,902
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/257,876
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/260,718
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/284,591
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 352
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 257
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TagMan PCR
US-10-025-806-257

Query Match 60.0%; Score 12; DB 16; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGCCACTCCCA 15
DB 5 TTGCCACTCCCA 16

RESULT 41
US-10-813-638-478/c
Sequence 478, Application US/10813638
Publication No. US20040235026A1
GENERAL INFORMATION:
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND M-
FILE REFERENCE: 15966-599
CURRENT APPLICATION NUMBER: US/10/813,638
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: 60/163,783
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1468
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 478
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (26)...(0)
OTHER INFORMATION: single nucleotide polymorphism
FEATURE:


```
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Accession number cg44005525
US-10-813-638-478
```

```
Query Match
Best Local Similarity 100.0%; Score 12; DB 20; Length 51;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GCATGCCACTC 12
Db 27 GCATGCCACTC 16
```

```
RESULT 42
US-09-908-975-15069/c
Sequence 15069, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: MASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: PAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15069
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-15069
```

```
Query Match
Best Local Similarity 100.0%; Score 12; DB 10; Length 60;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 9 ACTCCCATCTT 20
Db 17 ACTCCCATCTT 6
```

```
RESULT 43
US-09-908-975-17268
Sequence 17268, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: MASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: PAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17268
LENGTH: 60
```

```
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-17268
```

```
Query Match
Best Local Similarity 100.0%; Score 12; DB 10; Length 60;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GCATGCCACTC 12
Db 44 GCATGCCACTC 55
```

```
RESULT 44
US-10-257-017B-14061/c
Sequence 14061, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Christian Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 14061
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003215
US-10-257-017B-14061
```

```
Query Match
Best Local Similarity 100.0%; Score 11; DB 20; Length 13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 9 ACTCCCATCTT 19
Db 13 ACTCCCATCTT 3
```

```
RESULT 45
US-10-257-017B-14062
Sequence 14062, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 14062
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003215
US-10-257-017B-14062
```

```
Query Match
Best Local Similarity 100.0%; Score 11; DB 20; Length 13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 9 ACTCCCATCTT 19
Db 1 ACTCCCATCTT 11

Search completed: September 14, 2005, 11:54:03
Job time : 484 secs